

**TABLE 1: GENES IN THE APPLICATION****HMP:**

Nucleic Acid <u>SEQ ID NO</u>	Amino Acid <u>SEQ ID NO</u>	Identification Code <u>SEQ ID NO</u>	Contig. <u>NT Start</u>	<u>NT Stop</u>	Function
1 2	RXS02735	VV0074	14576	15280	6-Phosphogluco-lactonase
3 4	RXA01626	GR00452	4270	3926	L-ribulose-phosphate 4-epimerase
5 6	RXA02245	GR00554	13639	14295	RIBULOSE-PHOSPHATE 3-EPIMERASE (EC 5.1.3.1)
7 8	RXA01015	GR00290	346	5	RIBOSE 5-PHOSPHATE ISOMERASE (EC 5.3.1.6)

**TCA:**

Nucleic Acid <u>SEQ ID NO</u>	Amino Acid <u>SEQ ID NO</u>	Identification Code <u>SEQ ID NO</u>	Contig. <u>NT Start</u>	<u>NT Stop</u>	Function
9 10	RXN01312	VV0082	20803	18785	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
11 12	F RXA01312	GR00380	2690	1614	SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT (EC 1.3.99.1)
13 14	RXN00231	VV0083	15484	14015	SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP <sup>+</sup> ) (EC 1.2.1.16)
15 16	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
17 18	RXA01535	GR00427	1354	2760	FUMARATE HYDRATASE PRECURSOR (EC 4.2.1.2)
19 20	RXA00517	GR00131	1407	2447	MALATE DEHYDROGENASE (EC 1.1.1.37) (EC 1.1.1.82)
21 22	RXA01350	GR00392	1844	2827	MALATE DEHYDROGENASE (EC 1.1.1.37)

**EMB-Pathway**

Nucleic Acid <u>ID NO</u>	Amino Acid <u>SEQ ID NO</u>	Identification Code <u>SEQ ID NO</u>	Contig. <u>NT Start</u>	<u>NT Stop</u>	Function
23 24	RXA02149	GR00639	17786	18754	GLUCOKINASE (EC 2.7.1.2)
25 26	RXA01814	GR00515	2571	910	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
27 28	RXN02803	VV0086	1	657	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
29 30	F RXA02803	GR00784	2	400	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
31 32	RXN03076	VV0043	1624	35	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
33 34	F RXA02854	GR10002	1588	5	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
35 36	RXA00511	GR00129	1	513	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code Contig.	NT Start	NT Stop	Function	
37	38	RXN01365	VV0091	1476	103	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
39	40	F RXA01365	GR00397	897	4	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (EC 5.3.1.9) (EC 5.4.2.8)
	41	42	RXA00098	GR00014	6525	PHOSPHOGLUCOMUTASE (EC 5.4.2.2) / PHOSPHOMANNOMUTASE (EC 5.4.2.8)
	43	44	RXA01989	GR00578	1	GLUCOSE-6-PHOSPHATE ISOMERASE A (GPI A) (EC 5.3.1.9)
	45	46	RXA00340	GR00059	1549	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
	47	48	RXA02492	GR00720	2201	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
	49	50	RXA00381	GR00082	1451	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
	51	52	RXA02122	GR00636	6511	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
	53	54	RXA00206	GR00032	6171	6-PHOSPHOFRUCTOKINASE (EC 2.7.1.11)
	55	56	RXA01243	GR00359	2302	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
	57	58	RXA01882	GR00538	1165	1-PHOSPHOFRUCTOKINASE (EC 2.7.1.56)
	59	60	RXA01702	GR00479	1397	FRUCTOSE-BISPHOSPHATE ALDOLASE (EC 4.1.2.13)
	61	62	RXA02258	GR00654	26451	TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1)
	63	64	RXN01225	VV0064	6382	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
	65	66	F RXA01225	GR00354	5302	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE HOMOLOG
	67	68	RXA02256	GR00654	23934	GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
	69	70	RXA02257	GR00654	25155	PHOSPHOGLYCERATE 3-PHOSPHATE DEHYDROGENASE (EC 2.7.2.3)
	71	72	RXA00235	GR00036	2365	ENOLASE (EC 4.2.1.11)
	73	74	RXA01093	GR00306	1552	PYRUVATE KINASE (EC 2.7.1.40)
	75	76	RXN02675	VV0098	72801	PYRUVATE KINASE (EC 2.7.1.40)
	77	78	F RXA02675	GR00754	2	PYRUVATE KINASE (EC 2.7.1.40)
	79	80	RXA02695	GR00755	2949	PYRUVATE KINASE (EC 2.7.1.40)
	81	82	RXA0682	GR00179	5299	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
	83	84	RXA0683	GR00179	6440	PHOSPHOENOLPYRUVATE SYNTHASE (EC 2.7.9.2)
	85	86	RXN00635	VV0135	22708	PYRUVATE DEHYDROGENASE CYTOCHROME (EC 1.2.2.2)
	87	88	F RXA02807	GR00788	88	PYRUVATE DEHYDROGENASE CYTOCHROME (EC 1.2.2.2)
	89	90	F RXA00635	GR00167	3	PYRUVATE DEHYDROGENASE CYTOCHROME (EC 1.2.2.2)
	91	92	RXN03044	VV0019	1391	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
	93	94	F RXA02852	GR00852	3	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
	95	96	F RXA00268	GR00041	125	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
	97	98	RXN03086	VV0049	2243	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
	99	100	F RXA02887	GR10022	411	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
	101	102	RXN03043	VV0019	1	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
	103	104	F RXA02997	GR10039	1291	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
	105	106	RXN03083	VV0047	88	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
	107	108	F RXA02853	GR10001	89	DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
	109	110	RXA02259	GR00654	27401	PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
	111	112	RXN02326	VV0047	4500	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
	113	114	F RXA02326	GR00668	5338	PYRUVATE CARBOXYLASE
	115	116	RXN02327	VV0047	3533	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
	117	118	F RXA02327	GR00668	6305	PYRUVATE CARBOXYLASE
	119	120	RXN02328	VV0047	1842	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
	121	122	F RXA02328	GR00668	7783	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
	123	124	RXN01048	VV0079	12539	MALIC ENZYME (EC 1.1.1.39)
					111316	

Nucleic Acid <u>SEQ ID NO</u>	Amino Acid <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
125	126	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
127	128	F RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
129	130	RXA02694	GR00755	1879	2820	L-LACTATE DEHYDROGENASE (EC 1.1.1.27)
131	132	RXN00296	VV0176	35763	38606	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4)
133	134	F RXA00296	GR00048	3	2837	D-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.4)
135	136	RXA01901	GR00544	4158	5417	L-LACTATE DEHYDROGENASE (CYTOCHROME) (EC 1.1.2.3)
137	138	RXN01952	VV0105	9954	11666	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
139	140	F RXA01952	GR00562	1	216	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
141	142	F RXA01955	GR00562	4611	6209	D-LACTATE DEHYDROGENASE (EC 1.1.1.28)
143	144	RXA00293	GR00047	2645	1734	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
145	146	RXN01130	VW0157	6138	5536	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
147	148	F RXA01130	GR00315	2	304	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
149	150	RXN03112	VV0085	509	6	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
151	152	F RXA01133	GR00316	568	1116	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
153	154	RXN00871	VW0127	3127	2240	IOLB PROTEIN
155	156	F RXA00871	GR00239	2344	3207	IOLB PROTEIN: D-FRUCTOSE 1,6-BISPHOSPHATE = GLYCERONE-CC PHOSPHATE + D-GLYCERALDEHYDE 3-PHOSPHATE.
157	158	RXN02829	VV0354	287	559	IOLS PROTEIN
159	160	F RXA02829	GR00816	287	562	IOLS PROTEIN
161	162	RXN01468	VW0019	7474	8298	NAGD PROTEIN
163	164	F RXA01468	GR00422	1250	2074	PUTATIVE N-GLYCAL DEHYDROPHOTTRANSFERASE
165	166	RXA00794	GR00211	3993	2989	GLPX PROTEIN
167	168	RXN02920	VV0213	6135	5224	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
169	170	F RXA02379	GR00690	1390	686	D-3-PHOSPHOGLYCERATE DEHYDROGENASE (EC 1.1.1.95)
171	172	RXN02688	VV0098	59053	58385	PHOSPHOGLYCERATE MUTASE (EC 5.4.2.1)
173	174	RXN03087	VW0052	3216	3428	PYRUVATE CARBOXYLASE (EC 6.4.1.1)
175	176	RXN03186	VW0377	310	519	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
177	178	RXN03187	VV0382	3	281	PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
179	180	RXN02591	VV0098	14370	12541	PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP] (EC 4.1.1.32)
181	182	RXS01260	VW0009	3477	2296	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)
183	184	RXS01261	VV0009	3703	3533	LIPOAMIDE DEHYDROGENASE COMPONENT (E3) OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE COMPLEX (EC 1.8.1.4)

## Glycerol metabolism

Nucleic Acid <u>SEQ ID NO</u>	Amino Acid <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
185	186	RXA02640	GR00749	1400	2926	GLYCEROL KINASE (EC 2.7.1.30)
187	188	RXN01025	VW0143	5483	4488	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+) (EC 1.1.1.94)
189	190	F RXA01025	GR00293	939	1853	GLYCEROL-3-PHOSPHATE DEHYDROGENASE (NAD(P)+) (EC 1.1.1.94)
191	192	RXA01851	GR00525	3515	1830	AEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE (EC 1.1.99.5)
193	194	RXA01242	GR00359	1526	2302	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
195	196	RXA02288	GR00661	992	147	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR

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197 198	RXN01891	VV0122	24949	24086		GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
199 200	F RXA01891	GR00541	1736	918		GLYCEROL-3-PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
201 202	RXA02414	GR00703	3808	3062		Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
203 204	RXN01580	VV0122	22091	22807		Glycerophosphoryl diester phosphodiesterase

### Acetate metabolism

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
205 206	RXA01436	GR00418	2547	1357		ACETATE KINASE (EC 2.7.2.1)
207 208	RXA00686	GR00179	8744	7941		ACETATE OPERON REPRESSOR
209 210	RXA00246	GR00037	4425	3391		ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
211 212	RXA01571	GR00438	1360	1959		ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
213 214	RXA01572	GR00438	1928	2419		ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
215 216	RXA01758	GR00498	3961	2945		ALCOHOL DEHYDROGENASE (EC 1.1.1.1)
217 218	RXA02539	GR00726	11676	10159		ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
219 220	RXN03061	VV0034	108	437		ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
221 222	RXN03150	VV0155	10678	10055		ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
223 224	RXN0340	VW0033	3	860		ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
225 226	RXN01498	VW0008	1598	3160		ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
227 228	RXN02674	VV0315	15614	14163		ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
229 230	RXN00868	VV0127	2230	320		ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
231 232	RXN01143	VV0077	9372	8254		ACETOLACTATE SYNTHASE LARGE SUBUNIT (EC 4.1.3.18)
233 234	RXN01146	VW0264	243	935		ACETOLACTATE SYNTHASE SMALL SUBUNIT (EC 4.1.3.18)
235 236	RXN01144	VV0077	8237	7722		

### Butanediol, diacetyl and acetoin formation

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
237 238	RXA02474	GR00715	8082	7309		(S,S)-butane-2,3-diol dehydrogenase (EC 1.1.1.76)
239 240	RXA02453	GR00710	6103	5351		ACETOIN(DIACETYL) REDUCTASE (EC 1.1.1.5)
241 242	RXS01758	VV0112	27383	28399		ALCOHOL DEHYDROGENASE (EC 1.1.1.1)

**HMP-Cycle**

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
243 244	RXA02737	GR00763	3312	1771	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49)	
245 246	RXA02738	GR00763	4499	3420	TRANSALDOLASE (EC 2.2.1.2)	
247 248	RXA02739	GR00763	6769	4670	TRANSKETOLASE (EC 2.2.1.1)	
249 250	RXA00965	GR00270	1232	510	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)	
251 252	RXN00999	VV0106	2817	1366	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)	
253 254	F RXA00999	GR00283	3012	4448	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING (EC 1.1.1.44)	

**Nucleotide sugar conversion**

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
255 256	RXN02596	VV0098	48784	47582	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)	
257 258	F RXA02596	GR00742	1	489	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)	
259 260	F RXA02642	GR00749	5383	5880	UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9)	
261 262	RXA02572	GR00737	2	646	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)	
263 264	RXA02485	GR00718	2345	3445	UDP-N-ACETYL- <i>N</i> -OLIGORYUVOGLUCOSAMINE REDUCTASE (EC 1.1.1.158)	
265 266	RXA01216	GR00352	2302	1202	UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE (EC 2.7.7.23)	
267 268	RXA01259	GR00367	987	130	UTP-GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9)	
269 270	RXA01228	GR00616	573	998	UTP-GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (EC 2.7.7.9)	
271 272	RXA01262	GR00367	8351	7191	GDP-MANNOSE 6-DEHYDROGENASE (EC 1.1.1.132)	
273 274	RXA01377	GR00400	3935	5020	MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE (EC 2.7.7.13)	
275 276	RXA02063	GR00626	3301	4527	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (EC 2.7.7.27)	
277 278	RXN00014	VV0048	8848	9627	GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2.7.7.24)	
279 280	F RXA00014	GR00002	4448	5227	GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2.7.7.24)	
281 282	RXA01570	GR00438	427	1281	GLUCOSE-1-PHOSPHATE THYMIDYLYLTRANSFERASE (EC 2.7.7.24)	
283 284	RXA02666	GR00753	7260	6493	D-RIBITOL-5-PHOSPHATE CYTIDYLYLTRANSFERASE (EC 2.7.7.40)	
285 286	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)	

**Inositol and ribitol metabolism**

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
287	RXA01887	GR00539	4219	3209	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)	

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289	290	RXNC0013	VV0048	7966	8838	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATE 1 (EC 3.1.3.25)
291	292	F RXA00013	GR00002	3566	4438	MYO-INOSITOL-1(OR 4)-MONOPHOSPHATE 1 (EC 3.1.3.25)
293	294	RXA01099	GR00306	6328	5504	INOSITOL MONOPHOSPHATE PHOSPHATASE
295	296	RXN01332	VV0273	579	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
297	298	F RXA01332	GR00388	552	4	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
299	300	RXA01632	GR00454	2338	3342	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
301	302	RXA01633	GR00454	3380	4462	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
303	304	RXN01406	VV0278	2999	1977	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
305	306	RXN01630	VV0050	48113	47037	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
307	308	RXN00528	VV0079	23406	22318	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4)
309	310	RXN03057	VV0028	7017	7688	MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
311	312	F RXA02902	GR10040	10277	10948	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
313	314	RXA00251	GR00038	931	224	RIBITOL 2-DEHYDROGENASE (EC 1.1.1.56)

## Utilization of sugars

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
315	316	RXN02654	VV0090	12206	13090	GLUCOSE 1-DEHYDROGENASE (EC 1.1.1.47)
317	318	F RXA02654	GR00752	7405	8289	GLUCOSE 1-DEHYDROGENASE II (EC 1.1.1.47)
319	320	RXN01049	VV0079	9633	11114	GLUCONOKINASE (EC 2.7.1.12)
321	322	F RXA01049	GR00296	1502	492	GLUCONOKINASE (EC 2.7.1.12)
323	324	F RXA01050	GR00296	1972	1499	GLUCONOKINASE (EC 2.7.1.12)
325	326	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR
327	328	RXN00872	VV0127	6557	5604	FRUCTOKINASE (EC 2.7.1.4)
329	330	F RXA00872	GR00240	565	1086	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR
331	332	RXN00799	VV0009	58477	56834	(EC 3.2.1.2) (EC 3.2.1.37)
333	334	F RXA00799	GR00214	1	1584	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR
335	336	RXA0032	GR00003	12028	10520	(EC 3.2.1.2) (EC 3.2.1.37)
337	338	RXA02528	GR00725	6880	7854	MANNITOL 2-DEHYDROGENASE (EC 1.1.1.67)
339	340	RXN00316	VV0006	7035	8180	FRUCTOSE REPRESSOR
341	342	F RXA00309	GR00053	316	5	Hypothetical Oxidoreductase (EC 1.1.1.-)
343	344	RXN00310	VV0006	6616	7050	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
345	346	F RXA00310	GR00053	735	301	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
347	348	RXA00041	GR00007	1246	5	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
349	350	RXA02026	GR00615	725	6	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26)
351	352	RXA02061	GR00626	1842	349	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)
353	354	RXN01369	VV0124	595	1776	

Nucleic Acid	SEQ ID NO	Amino Acid	SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
355	356	F RXA01369	GR00398	3	503	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)		
357	358	F RXA01373	GR00399	595	1302	MANNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8)		
359	360	RXA02611	GR00743	1	1752	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)		
361	362	RXA02612	GR00743	1793	3985	1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18)		
363	364	RXN01884	VV0184	1	1890	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33)		
365	366	F RXA01884	GR00539	3	1475	GLYCOGEN DEBRANCHING ENZYME (EC 2.4.1.25) (EC 3.2.1.33)		
367	368	RXA01111	GR00306	16981	17427	GLYCOGEN OPERON PROTEIN GLGX (EC 3.2.1.-)		
369	370	RXN01550	VV0143	14749	16260	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)		
371	372	F RXA01550	GR00431	3	1346	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)		
373	374	RXN02100	VV0318	2	2326	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)		
375	376	F RXA02100	GR00631	3	920	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)		
377	378	F RXA02113	GR00633	2	1207	GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)		
379	380	RXA02147	GR00639	15516	16332	ALPHA-AMYLASE (EC 3.2.1.1)		
381	382	RXA01478	GR00422	10517	12352	GLUCOAMYLASE G1 AND G2 PRECURSOR (EC 3.2.1.3)		
383	384	RXA01888	GR00539	4366	4933	GLUCOSE-RESISTANCE AMYLASE REGULATOR		
385	386	RXN01927	VV0127	50623	49244	XYLULOSE KINASE (EC 2.7.1.17)		
387	388	F RXA01927	GR00555	3	1118	XYLULOSE KINASE (EC 2.7.1.17)		
389	390	RXA02797	GR00762	747	4	RIBOKINASE (EC 2.7.1.15)		
391	392	RXA02797	GR00778	1739	2641	RIBOKINASE (EC 2.7.1.15)		
393	394	RXA02730	GR00762	1768	731	RIBOSE OPERON REPRESSOR		
395	396	RXA02551	GR00729	2193	2552	6-PHOSPHO-BETA-GLUCOSIDASE (EC 3.2.1.86)		
397	398	RXA01325	GR00385	5676	5005	DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4)		
399	400	RXA00195	GR00030	543	1103	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-)		
401	402	RXA00196	GR00030	1094	1708	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.-)		
403	404	RXN01562	VV0191	1230	3137	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE		
405	406	F RXA01562	GR00436	2	1039	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE		
407	408	F RXA01705	GR00480	971	1573	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE		
409	410	RXN00879	VV0099	8763	6646	4-ALPHA-GLUCANO-TRANSFERASE (EC 2.4.1.25)		
411	412	F RXA00879	GR00242	5927	3828	4-ALPHA-GLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)		
413	414	RXN00043	VV0119	3244	2081	N-ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25)		
415	416	F RXA00043	GR00007	3244	2081	N-ACETYLGLUCOSAMYL TRANSFERASE (EC 2.4.1.-)		
417	418	RXN01752	VV0127	35265	33805	N-ACETYLGLUCOSAMYL TRANSFERASE (EC 2.4.1.-)		
419	420	F RXA01839	GR00520	1157	510	N-ACETYLGLUCOSAMYL TRANSFERASE (EC 2.4.1.-)		
421	422	RXA01859	GR00529	1473	547	GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10)		
423	424	RXA00042	GR00007	2037	1279	GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (EC 2.6.1.16)		
425	426	RXA01482	GR00422	17271	15397	URONATE ISOMERASE (EC 5.3.1.12)		
427	428	RXN03179	VV0336	2	667	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)		
429	430	F RXA02872	GR10013	675	4	URONATE ISOMERASE (EC 5.3.1.12)		
431	432	RXN03180	VV0337	672	163	URONATE ISOMERASE, Glucuronate isomerase (EC 5.3.1.12)		
433	434	F RXA02873	GR10014	672	163	GALACTOSIDE O-ACETYLTRANSFERASE (EC 2.3.1.18)		
435	436	RXA02292	GR00662	1611	2285	D-RIBITOL-5-PHOSPHATE CYTIDYLTRANSFERASE (EC 2.7.7.40)		
437	438	RXA02666	GR00753	7260	6493	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR		
439	440	RXA00202	GR00032	1216	275	D-RIBOSE-BINDING PERIPLASMIC PROTEIN PRECURSOR		
441	442	RXA02440	GR00709	5097	4258	dTDP-4-DEHYDRORHAMNOSE REDUCTASE (EC 1.1.1.33)		
443	444	RXN01569	VV0009	41086	42444			

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
445	446	F RXA01569	GR00438	2	427	DTDP-4-DEHYDRO-RHAMNOSE REDUCTASE (EC 1.1.1.13)
447	448	F RXA02055	GR00624	7122	8042	DTDP-4-DEHYDRO-RHAMNOSE REDUCTASE (EC 1.1.1.13)
449	450	RXA00825	GR00222	222	1154	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
451	452	RXA02054	GR00624	6103	7119	DTDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46)
453	454	RXN00427	VW0112	7004	6219	dTDP-RHAMNOSE-6-PHOSPHATE ISOMERASE RFBF (EC 2.---)
455	456	F RXA00427	GR00098	1591	2022	D TDP-RHAMNOSEYL TRANSFERASE RFBF (EC 2.---)
457	458	RXA00327	GR00057	10253	9880	PROTEIN ARAJ
459	460	RXA00328	GR00057	11147	10656	PROTEIN ARAJ
461	462	RXA00329	GR00057	12390	11167	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR (EC 3.2.1.39)
463	464	RXN01554	VW0135	28686	26545	UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
465	466	RXN03015	VW0063	289	8	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.---)
467	468	RXN03056	VW0028	6258	6935	PERIPLASMIC BETA-GLUCOSIDASE/BETA-XYLOSIDASE PRECURSOR
469	470	RXN03030	VW0009	57006	56443	(EC 3.2.1.37)
471	472	RXN00401	VW0025	12427	11489	5-DEHYDRO-4-DEOXYGLUCARATE DEHYDRATASE (EC 4.2.1.41)
473	474	RXN02125	VW0102	23242	22442	ALDOSE REDUCTASE (EC 1.1.1.21)
475	476	RXN00200	VW0181	1679	5116	arabinosyltransferase subunit B (EC 2.4.2.-)
477	478	RXN01175	VW0017	39688	38303	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
479	480	RXN01376	VW0091	5610	4750	PUTATIVE GLYCOSYL TRANSFERASE WBIF
481	482	RXN01631	VW0050	47021	46143	PUTATIVE HEXULOSE-6-PHOSPHATE ISOMERASE (EC 5.---)
483	484	RXN01593	VW0229	13274	12408	NAGD PROTEIN
485	486	RXN00337	VW0197	20369	21418	GALACTOKINASE (EC 2.7.1.6)
487	488	RXS00584	VW0323	5516	6640	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
489	490	RKS02574				BETA-HEXOSAMINIDASE A PRECURSOR (EC 3.2.1.52)
491	492	RXS003215				GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
493	494	F RXA01915	GR00549	1	1008	GLUCOSE-FRUCTOSE OXIDOREDUCTASE PRECURSOR (EC 1.1.99.28)
495	496	RXS03224				CYCLOMALTODEXTRINASE (EC 3.2.1.54)
497	498	F RXA00038	GR00006	1417	260	CYCLOMALTODEXTRINASE (EC 3.2.1.54)
		RXC00233				protein involved in sugar metabolism
		RXC00236				Membrane Lipoprotein involved in sugar metabolism
		RXC00271				Exported Protein involved in ribose metabolism
		RXC00338				protein involved in sugar metabolism
		RXC00362				Membrane Spanning Protein involved in metabolism of diols
		RXC00412				Amino Acid ABC Transporter ATP-Binding Protein involved in sugar metabolism
511	512	RXC00526				ABC Transporter ATP-Binding Protein involved in sugar metabolism
513	514	RXC01004				Membrane Spanning Protein involved in sugar metabolism
515	516	RXC01017				Cytosolic Protein involved in sugar metabolism
517	518	RXC01021				Cytosolic Kinase involved in metabolism of sugars and thiamin
519	520	RXC01212				ABC Transporter ATP-Binding Protein involved in sugar metabolism
521	522	RXC01306				Membrane Spanning Protein involved in sugar metabolism
523	524	RXC01366				Cytosolic Protein involved in sugar metabolism
525	526	RXC01372				Cytosolic Protein involved in sugar metabolism
527	528	RXC01659				protein involved in sugar metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code SEQ ID NO	Contig	NT Start	NT Stop	Function
529	530	RXC01663				protein involved in sugar metabolism
531	532	RXC01693				protein involved in sugar metabolism
533	534	RXC01703				Cytosolic Protein involved in sugar metabolism
535	536	RXC02254				Membrane Associated Protein involved in sugar metabolism
537	538	RXC02255				Cytosolic Protein involved in sugar metabolism
539	540	RXC02435				protein involved in sugar metabolism
541	542	F RXA02435	GR00709	825	268	Uncharacterized protein involved in glycerol metabolism (homolog of Drosophila rhomboid)
543	544	RXC03216				protein involved in sugar metabolism
<b>TCA-cycle</b>						
Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code SEQ ID NO	Contig	NT Start	NT Stop	Function
545	546	RXA02175	GR00641	10710	9418	CITRATE SYNTHASE (EC 4.1.3.7)
547	548	RXA02621	GR00746	2647	1829	CITRATE LYASE BETA CHAIN (EC 4.1.3.6)
549	550	RXN00519	VW0144	5585	3372	ISOCITRATE DEHYDROGENASE (NADP) (EC 1.1.1.42)
551	552	F RXA00521	GR00133	2	1060	ISOCITRATE DEHYDROGENASE [NADP] (EC 1.1.1.42)
553	554	RXN02209	VW0304	1	1671	ACONITATE HYDRATASE (EC 4.2.1.3)
555	556	F RXA02209	GR00648	3	1661	ACONITATE HYDRATASE (EC 4.2.1.3)
557	558	RXN02213	VW0305	1378	2151	ACONITATE HYDRATASE (EC 4.2.1.3)
559	560	F RXA02213	GR00649	1330	2046	ACONITATE HYDRATASE (EC 4.2.1.3)
561	562	RXA02056	GR00625	3	2870	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.2)
563	564	RXA01745	GR00495	2	1495	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
565	566	RXA00782	GR00206	3984	3103	SUCCINYL-COA SYNTHETASE ALPHA CHAIN (EC 6.2.1.5)
567	568	RXA00783	GR00206	5280	4009	SUCCINYL-COA SYNTHETASE BETA CHAIN (EC 6.2.1.5)
569	570	RXN01695	VW0139	11307	12806	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
571	572	F RXA01615	GR00449	8608	9546	L-MALATE DEHYDROGENASE (ACCEPTOR) (EC 1.1.99.16)
573	574	F RXA01695	GR00474	4388	4179	MALIC ENZYME (EC 1.1.1.39)
575	576	RXA00290	GR00046	4693	5655	MALIC ENZYME (EC 1.1.1.39)
577	578	RXN01048	VW0079	12539	11316	MALIC ENZYME (EC 1.1.1.39)
579	580	F RXA01048	GR00296	3	290	MALIC ENZYME (EC 1.1.1.39)
581	582	F RXA00290	GR00046	4693	5655	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
583	584	RXN03101	VW0066	2	583	DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT (E2) OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX (EC 2.3.1.61)
585	586	RXN02046	VW0025	15056	14640	oxoglutarate semialdehyde dehydrogenase (EC 1.2.1.-)
587	588	RXN00389	VW0025	11481	9922	

**Glyoxylate bypass**

<u>Nucleic Acid Seq ID NO</u>	<u>Amino Acid Seq ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
589	590	RXN02399	VV0176	19708	18365	ISOCITRATE LYASE (EC 4.1.3.1)
591	592	F RXA02399	GR00699	478	1773	ISOCITRATE LYASE (EC 4.1.3.1)
593	594	RXN02404	VV0176	20259	22475	MALATE SYNTHASE (EC 4.1.3.2)
595	596	F RXA02404	GR00700	3798	1663	MALATE SYNTHASE (EC 4.1.3.2)
597	598	RXA01089	GR00304	3209	3958	GLYOXYLATE-INDUCED PROTEIN
599	600	RXA01886	GR00539	3203	2430	GLYOXYLATE-INDUCED PROTEIN

**Methylcitrate-pathway**

<u>Nucleic Acid Seq ID NO</u>	<u>Amino Acid Seq ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
601	602	RXN03117	VV0092	3087	1576	2-methylisocitrate synthase (EC 5.3.3.-)
603	604	F RXA00406	GR00090	978	4	2-methylisocitrate synthase (EC 5.3.3.-)
605	606	F RXA00514	GR00130	1983	1576	2-methylisocitrate synthase (EC 5.3.3.-)
607	608	RXA00512	GR00130	621	4	2-methylisocitrate synthase (EC 4.1.3.31)
609	610	RXA00518	GR00131	3069	2773	2-methylisocitrate synthase (EC 4.1.3.31)
611	612	RXA01077	GR00300	4647	6017	2-methylisocitrate synthase (EC 5.3.3.-)
613	614	RXN03144	VV0141	2	901	2-methylisocitrate synthase (EC 5.3.3.-)
615	616	F RXA02322	GR00668	415	5	2-methylisocitrate synthase (EC 5.3.3.-)
617	618	RXA02329	GR00669	607	5	2-methylisocitrate synthase (EC 5.3.3.-)
619	620	RXA02332	GR00671	1906	764	2-methylisocitrate synthase (EC 4.1.3.31)
621	622	RXN02333	VV0141	901	1815	methylisocitrate lyase (EC 4.1.3.30)
623	624	F RXA02333	GR00671	2120	1902	methylisocitrate lyase (EC 4.1.3.30)
625	626	RXA00030	GR00003	9590	9979	LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5)

**Methyl-Malonyl-CoA-Mutases**

<u>Nucleic Acid Seq ID NO</u>	<u>Amino Acid Seq ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
627	628	RXN00148	VV0167	9849	12059	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
629	630	F RXA00148	GR00023	2002	5	METHYLMALONYL-COA MUTASE ALPHA-SUBUNIT (EC 5.4.99.2)
631	632	RXA00149	GR00023	3856	2009	METHYLMALONYL-COA MUTASE BETA-SUBUNIT (EC 5.4.99.2)

Redox Chain							
Others	Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function
633	634	RXN00317	VV0197	26879	27532	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)	
635	636	F RXA00317	GR00055	344	6	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)	
637	638	RXA02196	GR00645	3956	3264	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)	
639	640	RXN02461	VV0124	14236	14643	PHOSPHOGLYCOLATE PHOSPHATASE (EC 3.1.3.18)	
Others							
Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Config.	NT Start	NT Stop	Function	
641	642	RXN01744	VV0174	2350	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)	
643	644	F RXA00055	GR00008	11753	11890	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)	
645	646	F RXA01744	GR00494	2113	812	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I (EC 1.10.3.-)	
647	648	RXA00379	GR00082	212	6	CYTOCHROME C-TYPE BIOPENESIS PROTEIN CCDA	
649	650	RXA00385	GR00083	773	435	CYTOCHROME C-TYPE BIOPENESIS PROTEIN CCDA	
651	652	RXA01743	GR00494	806	6	CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT II (EC 1.10.3.-)	
653	654	RXN02480	VV0084	31222	29567	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)	
655	656	F RXA01919	GR00550	288	4	CYTOCHROME C OXIDASE SUBUNIT I (EC 1.9.3.1)	
657	658	F RXA02480	GR00717	1449	601	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)	
659	660	F RXA02481	GR00717	1945	1334	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)	
661	662	RXA02140	GR00639	7339	8415	CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1)	
663	664	RXA02142	GR00639	9413	10063	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1)	
665	666	RXA02144	GR00639	11025	12248	RIESKE IRON-SULFUR PROTEIN	
667	668	RXA02740	GR00763	7613	8542	PROBABLE CYTOCHROME C OXIDASE ASSEMBLY FACTOR	
669	670	RXA02743	GR00763	13534	12497	CYTOCHROME AA3 CONTROLLING PROTEIN	
671	672	RXA01227	GR00355	1199	1519	FERREROXIN	
673	674	RXA01865	GR00532	436	122	FERREROXIN	
675	676	RXA00680	GR00179	2632	2315	FERREROXIN VI	
677	678	RXA00679	GR00179	2302	1037	FERREROXIN-NAD(+)-REDUCTASE (EC 1.18.1.3)	
679	680	RXA00224	GR00032	24965	24015	ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT	
681	682	RXA00225	GR00032	25733	24998	ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT	
683	684	RXN00606	VV0192	11299	9026	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)	
685	686	F RXA00606	GR00160	121	1869	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)	
687	688	RXN00595	VV0192	8642	7113	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)	
689	690	F RXA00608	GR00160	2253	3017	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)	
691	692	RXA00913	GR00249	3	2120	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)	
693	694	RXA00909	GR00247	2552	3406	NADH DEHYDROGENASE I CHAIN L (EC 1.6.5.3)	
695	696	RXA00700	GR00182	846	43	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN <sup>2</sup>	
697	698	RXN00483	VV0086	44824	46287	NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR	
699	700	F RXA00483	GR00119	19106	20569	(EC 1.6.5.3) (EC 1.6.9.3)	
701	702	RXA01534	GR00427	1035	547	(EC 1.6.5.3) (EC 1.6.9.3)	
						NADH-DEPENDENT FMN OXYDOREDUCTASE	

Nucleic Acid <u>SEQ ID NO</u>	Amino Acid <u>SEQ ID NO</u>	Identification Code	Contig.	NT Start	NT Stop	Function
703	704	RXA00288	GR00046	2646	1636	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
705	706	RXA00741	GR00763	9585	8620	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
707	708	RXN00560	VV0101	9922	10788	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.9.-)
709	710	F RXA02560	GR00731	6339	7160	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.9.-)
711	712	RXA01311	GR00380	1611	865	SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN (EC 1.3.99.1)
713	714	RXN00314	VV0058	1273	368	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
715	716	F RXA00910	GR00248	3	1259	Hydrogenase subunits
717	718	RXN01895	VV0117	955	5	NADH DEHYDROGENASE (EC 1.6.99.3)
719	720	F RXA01895	GR00543	2	817	DEHYDROGENASE
721	722	RXA00703	GR00183	2556	271	FORMATE DEHYDROGENASE ALPHA CHAIN (EC 1.2.1.2)
723	724	RXN00705	VV0005	6111	5197	FDHD PROTEIN
725	726	F RXA00705	GR00184	1291	407	FDHD PROTEIN
727	728	RXN00388	VV0025	2081	3091	CYTOCHROME C BIOGENESIS PROTEIN CCSA
729	730	F RXA00388	GR00085	969	667	essential protein similar to cytochrome c
731	732	F RXA00386	GR00084	514	5	RESC PROTEIN, essential protein similar to cytochrome c biogenesis protein
733	734	RXA00945	GR00259	1876	2847	putative cytochrome oxidase
735	736	RXN00556	VV0101	5602	6759	FLAVOHEMOPROTEIN / DIHYDROPTERIDINE REDUCTASE (EC 1.6.99.7)
737	738	F RXA02556	GR00731	2019	3176	FLAVOHEMOPROTEIN
739	740	RXA01392	GR00408	2297	3373	GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18)
741	742	RXA00800	GR00214	2031	3134	GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (EC 1.2.1.1)
743	744	RXA02143	GR00639	10138	11025	QCRC PROTEIN, menaquinol:cytochrome c oxidoreductase
745	746	RXN03996	VV0058	405	4	NADH DEHYDROGENASE I CHAIN M (EC 1.6.5.3)
747	748	RXN00336	VV0176	32683	33063	NADH:UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3)
749	750	RXN02765	VV0317	3562	2794	Hypothetical Oxidoreductase
751	752	RXN02206	VV0302	1784	849	Hypothetical Oxidoreductase
753	754	RXN02554	VV0101	4633	4010	Hypothetical Oxidoreductase (EC 1.1.1.-)

### ATP-Synthase

Nucleic Acid <u>SEQ ID NO</u>	Amino Acid <u>SEQ ID NO</u>	Identification Code	Contig.	NT Start	NT Stop	Function
755	756	RXN01204	VV0121	1270	461	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
757	758	F RXA01204	GR00345	394	1155	ATP SYNTHASE A CHAIN (EC 3.6.1.34)
759	760	RXA01201	GR00344	675	2315	ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34)
761	762	RXN01193	VV0175	5280	3832	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
763	764	F RXA01193	GR00343	15	755	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
765	766	F RXA01203	GR00344	3355	3993	ATP SYNTHASE BETA CHAIN (EC 3.6.1.34)
767	768	RXN02821	VV0121	324	85	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
769	770	F RXA02821	GR00802	139	318	ATP SYNTHASE C CHAIN (EC 3.6.1.34)
771	772	RXA01200	GR00344	2	610	ATP SYNTHASE DELTA CHAIN (EC 3.6.1.34)
773	774	RXA01194	GR00343	770	1141	ATP SYNTHASE EPSILON CHAIN (EC 3.6.1.34)

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
775	776	RXA01202	GR00344	2375	3349	ATP SYNTHASE GAMMA CHAIN (EC 3.6.1.34)
777	778	RXN02434	WV0090	4923	3274	ATP-BINDING PROTEIN
<b>Cytochrome metabolism</b>						
<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
779	780	RXN00684	WV0005	29864	28581	CYTOCHROME P450 116 (EC 1.14.-:-)
781	782	RXN00387	WV0025	1150	2004	Hypothetical Cytochrome c Biogenesis Protein

**TABLE 2: GENES IDENTIFIED FROM GENBANK**

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvat carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-amino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	disR		Kimura, E. et al. "Molecular cloning of a novel gene, disR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	disR1; disR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	dyc	Pyruvate carboxylase	
AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeyer, L. et al. "The role of the <i>Corynebacterium glutamicum</i> rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetyl glutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in <i>Corynebacterium glutamicum</i> ," <i>Mol. Cells.</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the <i>Corynebacterium glutamicum</i> panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in <i>Escherichia coli</i> ," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinate; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete <sup>1</sup> )	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY; glnB; glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridyl)-removing enzyme; signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mqo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> ( <i>Brevibacterium lactofermentum</i> AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	tprL; tprE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1987244382-A 1 10/24/87
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diamino pelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diamino pelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotonuchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipiclorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776	Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93	
E05779	Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93	
E06110	Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93	
E06111	Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93	
E06146	Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93	
E06825	Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94	
E06826	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94	
E06827	Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94	
E07701	secY	Honno, N. et al. "Gene DNA participating in integration of membranous protein to membrane," Patent: JP 1994169780-A 1 06/21/94	
E08177	Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94	
E08178, E08179, E08180, E08181, E08182	Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94	
E08232	Acetohydroxy-acid isomerase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomerase," Patent: JP 1994277067-A 1 10/04/94	
E08234	secE	Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94	
E08643	FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95	
E08646	Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95	

GenBank™ Accession No.	Gene Name	Gene Function	Reference	
E08649	Aspartase	Kohana, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95		
E08900	Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95		
E08901	Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95		
E12594	Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-trypophan," Patent: JP 1997028391-A 1 02/04/97		
E12760. E12759.	transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97		
E12758				
E12764	Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97		
E12767	Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97		
E12770	aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97		
E12773	Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97		
E13655	Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97		
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)	
L07603	EC 4.2.1.15	3-deoxy-D-arabinohexulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinohexulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)	
L09232	IlvB; ilvN; ilvC	Acetylhydroxy acid synthase large subunit; Acetylhydroxy acid synthase small subunit; Acetylhydroxy acid isomerase/eductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
L35906	dxr	Diphtheria toxin repressor	Follette, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M13774		Prephenate dehydratase	Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16175	5S rRNA		Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M25819		Phosphoenolpyruvate carboxylase	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M85106		23S rRNA gene insertion sequence	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108	23S rRNA gene insertion sequence		Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992).
M89931	aecD; bmrQ; yhbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbw	Rossol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the bmrQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998).
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993).
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglM; cglIR; clgIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997).
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	objg; proB; unkdh	?gamma glutamyl kinase similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thiR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	cjpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5"-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the <i>lysA</i> gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepniew, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum fda</i> gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-biphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the <i>dapA</i> gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of lambda corynephage," <i>FEMS Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum lysA</i> gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum trpE</i> gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum threonine synthase gene</i> ," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075		Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of lambda corynephage," <i>FEMS Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene and in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmans, B.J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomeras," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum gdh</i> gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum lysI</i> gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cop1	Psi protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydridopicolinate reductase	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69103	csp2	Surface layer protein PS2	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X69104		IS3 related insertion element	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X70959	leuA	Isopropylmalate synthase	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X71489	icd	Isocitrate dehydrogenase (NADP+)	
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mirA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinschmidt, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Nocardia</i> and evidence for the evolutionary origin of the genus <i>Nocardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronemeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinyl-diaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of <i>Corynebacterium glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pia; ackA	Phosphate acetyltransferase; acetate kinase	Reinschmidt, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum pta</i> -ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marré, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE, lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xy B	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in <i>Corynebacterium glutamicum</i> and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> ( <i>Corynebacterium glutamicum</i> ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetyl muramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	prop	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of <i>Corynebacterium glutamicum glnA</i> gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Moreau, S. et al. "Analysis of the integration functions of &phi;304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21502	dapA; dapB	Dihydridopicolinate synthase; dihydridopicolinate reductase	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in <i>Brevibacterium lactofermentum</i> : Regulation of arg-S-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z29563	thrC	Threonine synthase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of <i>Brevibacterium lactofermentum</i> encodes dihydridopicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of <i>Brevibacterium lactofermentum</i> is coupled transcriptionally to the dtmR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in <i>Brevibacterium lactofermentum</i> : Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of <i>Brevibacterium lactofermentum ATCC 13869</i> ," <i>Gene</i> , 170(1):91-94 (1996)

A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	ATCC	NCIB	CECT	NCIC	DSMZ
Brevibacterium	ammoniagenes	21054						
Brevibacterium	ammoniagenes	19350						
Brevibacterium	ammoniagenes	19351						
Brevibacterium	ammoniagenes	19352						
Brevibacterium	ammoniagenes	19353						
Brevibacterium	ammoniagenes	19354						
Brevibacterium	ammoniagenes	19355						
Brevibacterium	ammoniagenes	19356						
Brevibacterium	ammoniagenes	21055						
Brevibacterium	ammoniagenes	21077						
Brevibacterium	ammoniagenes	21553						
Brevibacterium	ammoniagenes	21580						
Brevibacterium	ammoniagenes	39101						
Brevibacterium	butanicum	21196						
Brevibacterium	divaricatum	21792	P928					
Brevibacterium	flavum	21474						
Brevibacterium	flavum	21129						
Brevibacterium	flavum	21518						
Brevibacterium	flavum			B11474				
Brevibacterium	flavum			B11472				
Brevibacterium	flavum	21127						
Brevibacterium	flavum	21128						
Brevibacterium	flavum	21427						
Brevibacterium	flavum	21475						
Brevibacterium	flavum	21517						
Brevibacterium	flavum	21528						
Brevibacterium	flavum	21529						

Brevibacterium	flavum		B11477
Brevibacterium	flavum		B11478
Brevibacterium	flavum	21127	
Brevibacterium	flavum		B11474
Brevibacterium	heali	15527	
Brevibacterium	ketoglutamicum	21004	
Brevibacterium	ketoglutamicum	21089	
Brevibacterium	ketosoreductum	21914	
Brevibacterium	lactofermentum	70	
Brevibacterium	lactofermentum	74	
Brevibacterium	lactofermentum	77	
Brevibacterium	lactofermentum	21798	
Brevibacterium	lactofermentum	21799	
Brevibacterium	lactofermentum	21800	
Brevibacterium	lactofermentum	21801	
Brevibacterium	lactofermentum		B11470
Brevibacterium	lactofermentum		B11471
Brevibacterium	lactofermentum	21086	
Brevibacterium	lactofermentum	21420	
Brevibacterium	lactofermentum	21086	
Brevibacterium	lactofermentum	31269	
Brevibacterium	linens	9174	
Brevibacterium	linens	19391	
Brevibacterium	linens	8377	
Brevibacterium	paraffinolyticum		11160
Brevibacterium	spec.		717.73
Brevibacterium	spec.		717.73
Brevibacterium	spec.	14604	
Brevibacterium	spec.	21860	
Brevibacterium	spec.	21864	
Brevibacterium	spec.	21865	

<i>Brevibacterium</i>	spec.	21866
<i>Brevibacterium</i>	spec.	19240
<i>Corynebacterium</i>	<i>acetoacidophilum</i>	21476
<i>Corynebacterium</i>	<i>acetoacidophilum</i>	13870
<i>Corynebacterium</i>	<i>acetoglutamicum</i>	B11473
<i>Corynebacterium</i>	<i>acetoglutamicum</i>	B11475
<i>Corynebacterium</i>	<i>acetoglutamicum</i>	15806
<i>Corynebacterium</i>	<i>acetoglutamicum</i>	21491
<i>Corynebacterium</i>	<i>acetoglutamicum</i>	31270
<i>Corynebacterium</i>	<i>acetophilum</i>	B3671
<i>Corynebacterium</i>	<i>ammoniagenes</i>	6872
<i>Corynebacterium</i>	<i>ammoniagenes</i>	2399
<i>Corynebacterium</i>	<i>fujikense</i>	15511
<i>Corynebacterium</i>	<i>fujikense</i>	21496
<i>Corynebacterium</i>	<i>glutamicum</i>	14067
<i>Corynebacterium</i>	<i>glutamicum</i>	39137
<i>Corynebacterium</i>	<i>glutamicum</i>	21254
<i>Corynebacterium</i>	<i>glutamicum</i>	21255
<i>Corynebacterium</i>	<i>glutamicum</i>	31830
<i>Corynebacterium</i>	<i>glutamicum</i>	13032
<i>Corynebacterium</i>	<i>glutamicum</i>	14305
<i>Corynebacterium</i>	<i>glutamicum</i>	15455
<i>Corynebacterium</i>	<i>glutamicum</i>	13058
<i>Corynebacterium</i>	<i>glutamicum</i>	13059
<i>Corynebacterium</i>	<i>glutamicum</i>	13060
<i>Corynebacterium</i>	<i>glutamicum</i>	21492
<i>Corynebacterium</i>	<i>glutamicum</i>	21513
<i>Corynebacterium</i>	<i>glutamicum</i>	21526
<i>Corynebacterium</i>	<i>glutamicum</i>	21543
<i>Corynebacterium</i>	<i>glutamicum</i>	13287
<i>Corynebacterium</i>	<i>glutamicum</i>	21851
<i>Corynebacterium</i>	<i>glutamicum</i>	21253

Corynebacterium	glutamicum	21514
Corynebacterium	glutamicum	21516
Corynebacterium	glutamicum	21299
Corynebacterium	glutamicum	21300
Corynebacterium	glutamicum	39684
Corynebacterium	glutamicum	21488
Corynebacterium	glutamicum	21649
Corynebacterium	glutamicum	21650
Corynebacterium	glutamicum	19223
Corynebacterium	glutamicum	13869
Corynebacterium	glutamicum	21157
Corynebacterium	glutamicum	21158
Corynebacterium	glutamicum	21159
Corynebacterium	glutamicum	21355
Corynebacterium	glutamicum	31808
Corynebacterium	glutamicum	21674
Corynebacterium	glutamicum	21562
Corynebacterium	glutamicum	21563
Corynebacterium	glutamicum	21564
Corynebacterium	glutamicum	21565
Corynebacterium	glutamicum	21566
Corynebacterium	glutamicum	21567
Corynebacterium	glutamicum	21568
Corynebacterium	glutamicum	21569
Corynebacterium	glutamicum	21570
Corynebacterium	glutamicum	21571
Corynebacterium	glutamicum	21572
Corynebacterium	glutamicum	21573
Corynebacterium	glutamicum	21579
Corynebacterium	glutamicum	19049
Corynebacterium	glutamicum	19050

<i>Corynebacterium glutamicum</i>	19051
<i>Corynebacterium glutamicum</i>	19052
<i>Corynebacterium glutamicum</i>	19053
<i>Corynebacterium glutamicum</i>	19054
<i>Corynebacterium glutamicum</i>	19055
<i>Corynebacterium glutamicum</i>	19056
<i>Corynebacterium glutamicum</i>	19057
<i>Corynebacterium glutamicum</i>	19058
<i>Corynebacterium glutamicum</i>	19059
<i>Corynebacterium glutamicum</i>	19060
<i>Corynebacterium glutamicum</i>	19185
<i>Corynebacterium glutamicum</i>	13286
<i>Corynebacterium glutamicum</i>	21515
<i>Corynebacterium glutamicum</i>	21527
<i>Corynebacterium glutamicum</i>	21544
<i>Corynebacterium glutamicum</i>	21492
<i>Corynebacterium glutamicum</i>	B8183
<i>Corynebacterium glutamicum</i>	B8182
<i>Corynebacterium glutamicum</i>	B12416
<i>Corynebacterium glutamicum</i>	B12417
<i>Corynebacterium glutamicum</i>	B12418
<i>Corynebacterium glutamicum</i>	B11476
<i>Corynebacterium glutamicum</i>	21608
<i>Corynebacterium lilium</i>	P973
<i>Corynebacterium nitrilophilus</i>	21419
<i>Corynebacterium spec.</i>	11594
<i>Corynebacterium spec.</i>	P4445
<i>Corynebacterium spec.</i>	P4446
<i>Corynebacterium spec.</i>	31088
<i>Corynebacterium spec.</i>	31089
<i>Corynebacterium spec.</i>	31090
<i>Corynebacterium spec.</i>	31090

<i>Corynebacterium</i>	spec.	31090							
<i>Corynebacterium</i>	spec.	15954							20145
<i>Corynebacterium</i>	spec.	21857							
<i>Corynebacterium</i>	spec.	21862							
<i>Corynebacterium</i>	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Colección Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4<sup>th</sup> edn). World federation for culture collections world data center on microorganisms, Saimata, Japen.

**TABLE 4: ALIGNMENT RESULTS**

<u>ID #</u>	<u>length</u>	<u>Genbank Hit</u>	<u>Length</u>	<u>Accession</u>	<u>Name of Genbank Hit</u>	<u>Source of Genbank Hit</u>	<u>% homology</u>	<u>Date of Deposit</u>
	[N]						[GAP]	
rxa00013	996	GB_GSS4:AQ713475	581	AQ713475	HS_5402_B2_A12_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic Homo sapiens clone Plate=978 Col=24 Row=B, genomic survey sequence.	Drosophila melanogaster	37,148	13-Jul-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp. *** SEQUENCING IN PROGRESS *** , 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
		GB_HTG3:AC007420	130583	AC007420	Drosophila melanogaster chromosome 2 clone BACR07M10 (D630) RPCI-98 07.M.10 map 24A-24D strain y; cn bw sp. *** SEQUENCING IN PROGRESS*** , 83 unordered pieces.	Drosophila melanogaster	34,568	20-Sep-99
rxa00014	903	GB_BA1:MTCY3A2	25830	Z83867	Mycobacterium tuberculosis H37Rv complete genome; segment 136/162.	Mycobacterium tuberculosis	58,140	17-Jun-98
		GB_BA1:MLCB1779	43254	Z98271	Mycobacterium leprae cosmid B1779.	Mycobacterium leprae	57,599	8-Aug-97
		GB_BA1:SPURCLUS	9120	X92429	S.alboniger napH, purF, purT, purU, pur4, pur5 and pur3 genes.	Streptomyces anulatus	55,667	28-Feb-96
rxa00030	513	GB_EST21:C89713	767	C89713	C89713 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSG229 mRNA sequence.	Dictyostelium discoideum	45,283	20-Apr-98
		GB_EST28:AI497294	484	AI497294	fb6303.y1 Zebrafish WashU MIPMG EST Danio rerio cDNA 5' similar to SW-AFP4 MYOOC P80961 ANTIFREEZE PROTEIN LS-12 ; mRNA sequence.	Danio rerio	42,991	11-MAR-1999
		GB_EST21:C92167	637	C92167	C92167 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSD79 mRNA sequence.	Dictyostelium discoideum	44,444	12-Jul-99
rxa00032	1632	GB_BA2:AF010496	169370	AF010496	Rhodobacter capsulatus strain SB1003, partial genome.	Rhodobacter capsulatus	39,689	12-MAY-1998
		GB_BA2:AF018073	9810	AF018073	Rhodobacter sphaeroides operon regulator (smoC), periplasmic sorbitol-binding protein (smoE), sorbitol/mannitol transport inner membrane protein (smoF), sorbitol/mannitol transport ATP-binding transport protein (smoK), sorbitol dehydrogenase (smoS), mannitol dehydrogenase (mtk), and periplasmic mannitol-binding protein (smoT) genes, complete cds.	Rhodobacter sphaeroides	48,045	22-OCT-1997
		GB_BA2:AF045245	5930	AF045245	Klebsiella pneumoniae D-arabinitol transporter (dalT), D-arabinitol kinase (dalK), D- arabinitol dehydrogenase (dalD), and repressor (dalR) genes, complete cds.	Klebsiella pneumoniae	38,514	16-Jul-98
rxa00041	1342	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	99,031	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	99,031	07-OCT-1996 (Rel. 52, Created)
		GB_IN1:LMFL5883	31934	AL117384	Leishmania major Friedlin chromosome 23 cosmid L5883, complete sequence.	Leishmania major	43,663	21-OCT-1999 (Rel. 52, Created)
rxa00042	882	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	94,767	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patient US 5556776.	Unknown.	94,767	07-OCT-1996
		GB_IN1:CEU33051	4899	U33051	Caenorhabditis elegans sur-2 mRNA, complete cds.	Caenorhabditis elegans	40,276	23-Jan-96
		GB_PAT:I26124	6911	I26124	Sequence 4 from patient US 5556776.	Unknown.	97,591	07-OCT-1996
		EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	97,591	08-OCT-1997 (Rel. 52, Created)
		GB_PPR3:AC005174	39769	AC005174	Homo sapiens clone UWGC:g1564a012 from 7p14-15, complete sequence.	Homo sapiens	35,879	24-Jun-98

**TABLE 4: ALIGNMENT RESULTS**

rx00098 1743	GB_BA1:MSU88433	1928	U88433	Mycobacterium smegmatis phosphoglucose isomerase gene, complete cds.	<i>Mycobacterium smegmatis</i>	62,658	19-Apr-97
	GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	<i>Streptomyces coelicolor</i>	37,638	27-Jul-98
	GB_BA1:MTCY10D7	39800	279700	Mycobacterium tuberculosis H37Rv complete genome; segment 44/162.	<i>Mycobacterium tuberculosis</i>	36,784	17-Jun-98
	GB_BA1:MTCY277	38300	279701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	<i>Mycobacterium tuberculosis</i>	67,457	17-Jun-98
	GB_BA1:MSGY456	37916	AD000001	Mycobacterium tuberculosis sequence from clone y456.	<i>Mycobacterium tuberculosis</i>	40,883	03-DEC-1996
	GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175.	<i>Mycobacterium tuberculosis</i>	67,457	10-DEC-1996
	GB_BA1:MSGY456	37316	AD000001	Mycobacterium tuberculosis sequence from clone y456.	<i>Mycobacterium tuberculosis</i>	35,883	03-DEC-1996
	GB_BA1:MSGY175	18106	AD000015	Mycobacterium tuberculosis sequence from clone y175.	<i>Mycobacterium tuberculosis</i>	51,001	10-DEC-1996
	GB_BA1:MTCY277	38300	279701	Mycobacterium tuberculosis H37Rv complete genome; segment 65/162.	<i>Mycobacterium tuberculosis</i>	51,001	17-Jun-98
	GB_BA1:MTCY274	39891	274024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	<i>Mycobacterium tuberculosis</i>	35,735	19-Jun-98
	GB_BA1:MSGB529CS	36385	L78824	Mycobacterium leprae cosmid B1529 DNA sequence.	<i>Mycobacterium leprae</i>	57,014	15-Jun-96
	GB_BA1:MTCY274	39891	274024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	<i>Mycobacterium tuberculosis</i>	41,892	19-Jun-98
	GB_BA1:MTCY274	39891	274024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	<i>Mycobacterium tuberculosis</i>	41,841	19-Jun-98
	GB_BA1:MTCY274	39891	274024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	<i>Mycobacterium tuberculosis</i>	36,599	19-Jun-98
	GB_RORATCBRQ	10752	M55532	Rat carbohydrate binding receptor gene, complete cds.	<i>Rattus norvegicus</i>	36,212	27-Apr-93
	GB_EST11AA253618	313	AA253618	mw95cf10.1 Soares mouse NM_1. Mus musculus cDNA clone IMAGE:678450 5, mRNA sequence.	<i>Mus musculus</i>	38,816	13-MAR-1997
	GB_EST26AI390284	490	AI390284	mw96a03.y1 Soares mouse NM_1. Mus musculus cDNA clone IMAGE:678508 5' similar to TR:009171 009171 BETAINE-HOMOCYSTEINE METHYLTRANSFERASE,, mRNA sequence.	<i>Mus musculus</i>	42,239	2-Feb-98
	GB_EST26AI390280	467	AI390280	mw95c10.y1 Soares mouse NM_1. Mus musculus cDNA clone IMAGE:678450 5', mRNA sequence.	<i>Mus musculus</i>	37,307	2-Feb-99
	GB_BA1:MLCB637	44882	Z99263	Mycobacterium leprae cosmid B637.	<i>Mycobacterium leprae</i>	58,312	17-Sep-97
	GB_BA1:MTV012	70287	ALC021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	<i>Mycobacterium tuberculosis</i>	36,632	23-Jun-99
	GB_BA1:SC6E10	23990	AL109661	Streptomyces coelicolor cosmid 6E10.	<i>Streptomyces coelicolor A3(2)</i>	38,616	5-Aug-99
	GB_BA1:BU32230	1769	U32230	Bradyrhizobium japonicum electron transfer flavoprotein small subunit (etfS) nd large Bradyrhizobium japonicum subunit (etfL) genes, complete cds.	<i>Bradyrhizobium japonicum</i>	48,038	25-MAY-1996
	GB_BA1:PDEETFAB	2440	L14864	Paracoccus denitrificans electron transfer flavoprotein alpha and beta subunit genes, Paracoccus denitrificans complete cds's.	<i>Paracoccus denitrificans</i>	48,351	27-OCT-1993
	GB_HTC3:AC009689	177954	AC009689	Homo sapiens chromosome 4 clone 104_F_7 map 4, LOW-PASS SEQUENCE SAMPLING.	<i>Homo sapiens</i>	38,756	28-Aug-99
	GB_RO:AF060178	2057	AF060178	Mus musculus heparan sulfate 2-sulfotransferase (Hs2st) mRNA, complete cds.	<i>Mus musculus</i>	39,506	18-Jun-98
	GB_GSS11:AO325043	734	AQ325043	mgx0020/01r, genomic survey sequence.	<i>Magnaporthe grisea</i>	38,333	8-Jan-99
	GB_EST31:AI676413	551	AI676413	elmerEST01671/Elmera tenella cDNA clone elmerEST01671, mRNA sequence.	<i>Elmeria tenella</i>	35,542	19-MAY-1999
	GB_BA1:MTCY10G2	38970	Z92539	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162.	<i>Mycobacterium tuberculosis</i>	65,759	17-Jun-98
	GB_BA2:AF061753	3721	AF061753	Nitrosomonas europaea CTP synthase (pyG) gene, partial cds, and endbase (eno) gene, complete cds.	<i>Nitrosomonas europaea</i>	58,941	31-Aug-98
	GB_BA2:AF086791	37867	AF086791	Zymomonas mobilis strain ZM4 clone 67E10 carbamoylphosphate synthetase large subunit (carB), transcription elongation factor (greA), endbase (eno), pyruvate dehydrogenase alpha subunit (pdhA), pyruvate dehydrogenase beta subunit (pdhB), ribonuclease H (rnh), homoserine kinase homolog, alcohol dehydrogenase II (adhB), and excinuclease ABC subunit A (uvrA) genes, complete cds; and unknown genes.	<i>Zymomonas mobilis</i>	61,239	4-Nov-98
	GB_BA2:AF012550	2690	AF012550	Acinetobacter sp. BD413 ComP (comp) gene, complete cds.	<i>Acinetobacter</i> sp. BD413	53,726	27-Sep-99

**TABLE 4: ALIGNMENT RESULTS**

GB_PAT:E03856	1506	E03856	gDNA encoding alcohol dehydrogenase.	Bacillus stearothermophilus	51,688	29-Sep-97	
GB_BA1:BACADHT	1688	D90421	B. stearothermophilus adhT gene for alcohol dehydrogenase.	Bacillus stearothermophilus	51,602	7-Feb-99	
GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	42,875	17-Jun-98	
GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	40,380	18-Jun-98	
GB_BA1:MTV004	69350	AL009198	Mycobacterium tuberculosis H37Rv complete genome; segment 144/162.	Mycobacterium tuberculosis	41,789	18-Jun-98	
GB_BA2:AF050114	1038	AF050114	Pseudomonas sp. W7 alginate lyase gene, complete cds.	Pseudomonas sp. W7	49,898	03-MAR-1999	
GB_GSS33B16984	469	B16984	344A14.TVC CTT7978SKA1 Homo sapiens genomic clone A-344A14, genomic survey.	Homo sapiens	39,355	4-Jun-98	
GB_JN2:AF144549	7887	AF144549	Aedes albopictus ribosomal protein L34 (rp34) gene, complete cds.	Aedes albopictus	36,509	3-Jun-99	
GB_EST1:IT28483	313	T28483	EST#6182 Human Kidney Homo sapiens cDNA 3' end similar to flavin-containing monooxygenase 1 (HET-1956), mRNA sequence.	Homo sapiens	42,997	6-Sep-95	
GB_PR1:HUMFMO1	2134	M64082	Human flavin-containing monooxygenase (FMO1) mRNA, complete cds.	Homo sapiens	37,915	8-Nov-94	
GB_EST3:AI734238	512	AI734238	zb7305.y5 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:309224_5' similar to gb M64082 DIMETHYL ANILINE MONOOXYGENASE (HUMAN); mRNA sequence.	Homo sapiens	41,502	14-Jun-99	
rxa00296 2967	GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPC1-98 11.H20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 92 unordered pieces.	Drosophila melanogaster	33,890	02-DEC-1999
GB_EST15:AA531468	414	AA531468	nij63d12.s1 NCL_CGAP_Pr10 Homo sapiens cDNA clone IMAGE:987175, mRNA sequence.	Homo sapiens	40,821	20-Aug-97	
GB_HTG6:AC011069	168266	AC011069	Drosophila melanogaster chromosome X clone BACR11H20 (D881) RPC1-98 11.H20 map 12B-12C strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 92 unordered pieces.	Drosophila melanogaster	30,963	02-DEC-1999	
rxa00310 558	GB_VI:VMVY16780	186986	Y16780	variola minor virus complete genome.	variola minor virus	35,883	2-Sep-99
	GB_VI:VARCG	186103	L22579	Variola major virus (strain Bangladesh-1975) complete genome.	Variola major virus	34,864	12-Jan-95
	GB_VI:VVGAA	185578	X69198	Variola virus DNA complete genome.	Variola virus	36,000	13-DEC-1996
rxa00317 777	GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
	GB_HTG3:AC009571	159648	AC009571	Homo sapiens chromosome 4 clone 57_A_22 map 4, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces.	Homo sapiens	36,988	29-Sep-99
rxa00327 507	GB_PR3:AC005697	174503	AC005697	Homo sapiens chromosome 17, clone hRPK1_138_P_22, complete sequence.	Homo sapiens	36,340	09-OCT-1998
	GB_BA1:LCATPASEB	1514	X64542	L.casei gene for ATPase beta-subunit.	Lactobacillus casei	34,664	11-DEC-1992
	GB_BA1:LCATPASEB	1514	X64542	L.casei gene for ATPase beta-subunit.	Lactobacillus casei	39,308	11-DEC-1992
rxa00328 615	GB_BA1:STYPPUTPE	1887	L01138	Salmonella (S2980) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
	GB_BA1:STYPPUTPF	1887	L01139	Salmonella (S2983) proline permease (putP) gene, 5' end.	Salmonella sp.	39,623	09-MAY-1996
	GB_BA1:STYPPUTPI	1889	L01142	Salmonella (S3015) proline permease (putP) gene, 5' end.	Salmonella sp.	42,906	09-MAY-1996
rxa00329 1347	GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone D0740D02 from 7p14-p15, complete sequence.	Homo sapiens	38,142	16-MAY-1996
	GB_PR4:AC004916	129014	AC004916	Homo sapiens clone D10891L14, complete sequence.	Homo sapiens	38,549	17-Jul-99
	GB_PR3:AC004691	141990	AC004691	Homo sapiens PAC clone D0740D02 from 7p14-p15, complete sequence.	Homo sapiens	35,865	16-MAY-1996
rxa00340 1269	GB_BA1:MTCY427	38110	Z70692	Mycobacterium tuberculosis H37Rv complete genome; segment 99/162.	Mycobacterium tuberculosis	38,940	24-Jun-99
	GB_GSS12:AQ412290	238	AC412290	RPC1-11-195H2.TV RPC1-11 Homo sapiens genomic clone RPC1-11-195H2, genomic survey sequence.	Homo sapiens	36,555	23-MAR-1999
	GB_PL2:AF112871	2394	AF112871	Asiatica longa small subunit ribosomal RNA gene, complete sequence.	Asiatica longa	36,465	28-Jun-99

**TABLE 4: ALIGNMENT RESULTS**

rx00379 307	GB-HTG1:CEY56A3	224746 AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99
	GB-HTG1:CEY56A3	224746 AL022280	Caenorhabditis elegans chromosome III clone Y56A3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	35,179	6-Sep-99
	GB_PR2:HS134O19	86697 AL034555	Human DNA sequence from clone 134O19 on chromosome 1p36.11-36.33, complete sequence.	Homo sapiens	40,604	23-Nov-99
rx00381 729	GB_GSS4:AQ730532	416 AQ730532	HS_2149_A1_C06_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2149 Col=11 Row=E, genomic survey sequence.	Homo sapiens	35,766	15-Jul-99
	GB_EST23:AI120939	561 AI120939	ub74f05.r1 Soares mouse mammary gland NIMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:MI19381 Mouse calmodulin (MOUSE); mRNA sequence.	Mus musculus	41,113	2-Sep-98
	GB_EST23:AI120939	561 AI120939	ub74f05.r1 Soares mouse mammary gland NIMLMG Mus musculus cDNA clone IMAGE:1383489 5' similar to gb:J04046 CALMODULIN (HUMAN); gb:MI19381 Mouse calmodulin (MOUSE); mRNA sequence.	Mus musculus	41,113	2-Sep-98
rx00385 362	GB_EST32:AI1726450	565 AI1726450	BNLGH15857 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AF015913) Skb1Hs [Homo sapiens], mRNA sequence.	Gossypium hirsutum	41,152	11-Jun-99
	GB_GSS4:AQ740856	768 AQ740856	HS_2274_A2_A07_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2274 Col=14 Row=A, genomic survey sequence.	Homo sapiens	41,360	16-Jul-99
rx00388 1134	GB_PR1:HSPA1P	1587 X91809	H.sapiens mRNA for GAIP protein.	Homo sapiens	36,792	29-MAR-1996
	GB_BA1:MTY25D10	40838 Z95558	Mycobacterium tuberculosis H37Rv complete genome; segment 28/162.	Mycobacterium tuberculosis	51,852	17-Jun-98
	GB_BA1:MSGY224	40051 AD000004.	Mycobacterium tuberculosis sequence from clone y224.	Mycobacterium tuberculosis	51,852	03-DEC-1996
	GB-HTG1:AP000471	72466 AP000471	Hom sapiens chromosome 21 clone B2308H15 map 21q22.3, *** SEQUENCING IN HOM sapiens PROGRESS ***, in unordered pieces.	Hom sapiens	36,875	13-Sep-99
rx00427 909	GB_BA1:MSGY126	37164 AD000012	Mycobacterium tuberculosis sequence from clone y126.	Mycobacterium tuberculosis	60,022	10-DEC-1996
	GB_BA1:MTY13D12	37085 Z80343	Mycobacterium tuberculosis H37Rv complete genome; segment 156/162.	Mycobacterium tuberculosis	60,022	17-Jun-98
	GB-HTG1:CEY48C3	270193 Z98555	Caenorhabditis elegans chromosome II clone Y48C3, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	28,013	29-MAY-1999
rx00483 1587	GB_PR2:HSAF001550	173882 AF001550	Hom sapiens chromosome 16 BAC clone C1T987SK-334D11 complete sequence.	Homo sapiens	38,226	22-Aug-97
	GB_BA1:LICPJW565	12282 Y12736	Lactococcus lactis cremoris plasmid pJW556 DNA, abiiR genes and orfX.	Lactococcus lactis subsp. cremoris	37,492	01-MAR-1999
	GB-HTG2:AC006754	206217 AC006754	Caenorhabditis elegans clone Y40B10, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Caenorhabditis elegans	36,648	23-Feb-99
rx00511 615	GB_PR3:HSE127C11	38423 Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	39,831	23-Nov-99
	GB_PR3:HSE127C11	38423 Z74581	Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-qter contains STS.	Homo sapiens	36,409	23-Nov-99
rx00512 718	GB_BA1:MTCY22G8	22550 Z95585	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	56,232	17-Jun-98
	GB_BA1:MSGLTA	1776 X66513	M.smegmatis gltA gene for citrate synthase.	Mycobacterium smegmatis	56,143	20-Sep-91
	GB_BA2:ECU73857	128824 U73857	Escherichia coli chromosome minutes 6-8.	Escherichia coli	48,563	14-Jul-99
rx00517 1164	GB-HTG2:AC006911	298804 AC006911	Caenorhabditis elegans clone Y94H6X, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99
	GB-HTG2:AC006911	298804 AC006911	Caenorhabditis elegans clone Y94H6X, *** SEQUENCING IN PROGRESS ***, 15 unordered pieces.	Caenorhabditis elegans	37,889	24-Feb-99

**TABLE 4: ALIGNMENT RESULTS**

GB_EST29:AI602158	481	AI602158	UI-R-ABO-yy-a-0-UI_s2 UI-R-AB0 Rattus norvegicus cDNA clone UI-R-ABO-yy-a- Rattus norvegicus	40,833	21-Apr-99
rx00518	320	GB_BA2:ECU73857 GB_BA2:STU51879	128824 U73857 8371 U51879	Escherichia coli chromosome 6-8. Salmonella typhimurium propionate catabolism operon: RpN activator protein homolog (prpR), carboxyphosphonoenopyruvate phosphonotutase homolog (prpB), citrate synthase homolog (prpC), prpD and prpE genes, complete cds.	14-Jul-99 5-Aug-99
rx00606	2378	GB_BA2:AE000140 GB_EST32:AU068253 GB_EST13:AA363046 GB_EST32:AU068253 GB_BA1:PAORF1	12498 AE000140 376 AU068253 329 AA363046 376 AU068253 1440 X13378	Escherichia coli K-12 MG1655 section 30 of 400 of the complete genome. Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence. EST72922 Ovary II Homo sapiens cDNA 5' end, mRNA sequence. Rice callus Oryza sativa cDNA clone C12658_9A, mRNA sequence. Pseudomonas amyloferamosa DNA for ORF 1.	12-Nov-98 7-Jun-99 21-Apr-97 7-Jun-99 14-Jul-95
rx00635	1860	GB_BA1:PAORF1	1440 X13378	Pseudomonas amyloferamosa DNA for ORF 1.	Pseudomonas amyloferamosa 54,422
rx00679	1389	GB_PL2:AC010871	80381 AC010871	Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana 38,244
		GB_PL1:AT81KBGEN GB_PL2:AC010871	81493 X98130 80381 AC010871	A.thaliana 8 kb genomic sequence. Arabidopsis thaliana chromosome III BAC T16O11 genomic sequence, complete sequence.	Arabidopsis thaliana 36,091 Arabidopsis thaliana 37,135
rx00680	441	GB_PR3:AC004058 GB_PL1:AT81KBGEN GB_PL1:AB266648	38400 AC004058 81493 X98130 43481 AB266648	Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence. A.thaliana 8 kb genomic sequence. Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence.	Homo sapiens 36,165 Arabidopsis thaliana 38,732 Arabidopsis thaliana 38,732
rx00682	2022	GB_HTG3:AC010325	19710 AC010325	Homo sapiens chromosome 19 clone CITB-E1_25668A17, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens 37,976
		GB_HTG3:AC010325	19710 AC010325	Homo sapiens chromosome 19 clone CITB-E1_25668A17, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens 37,976
rx00683	1215	GB_PR4:AC008179 GB_BA2:AE000896	181745 AC008179 10707 AE000896	Homo sapiens clone NH0576F01, complete sequence. Methanobacterium thermoautotrophicum from bases 1189349 to 1200055 (section 102 of 148) of the complete genome.	Homo sapiens 37,143 Methanobacterium thermoautotrophicum 38,429
		GB_IN1:DMBR7A4 GB_ES135:AV163010	212734 AL109630 273 AV163010	Drosophila melanogaster clone BACR7A4. Mus musculus head C57BL/6J 13-day embryo Mus musculus cDNA cloneMus musculus 3110006122, mRNA sequence.	Drosophila melanogaster 36,454 Mus musculus 41,758
rx00686	927	GB_HTG2:HSDJ137K2	190223 AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING Homo sapiens IN PROGRESS ***, in unordered pieces.	30-Jul-99 8-Jul-99
		GB_HTG2:HSDJ137K2	190223 AL049820	Homo sapiens chromosome 6 clone RP1-137K2 map q25.1-25.3, *** SEQUENCING Homo sapiens IN PROGRESS ***, in unordered pieces.	03-DEC-1999
rx00700	927	GB_EST12:AA284399	431 AA284399	z57b04,r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701551 5, mRNA Homo sapiens sequence.	38,031
		GB_EST12:AA284399	431 AA284399	uj4d03,x1 Sugano mouse liver mRNA Mus musculus cDNA clone IMAGE:1922789 3' Mus musculus similar to gb:Z28407 60S RIBOSOMAL PROTEIN L8 (HUMAN); mRNA sequence.	38,031
		GB_EST134:AI785570	454 AI785570		39,205
		GB_EST134:AI785570	454 AI785570		14-Aug-97
					2-Jul-99
					41,943

TABLE 4: ALIGNMENT RESULTS

GB_EST25:AI256147	684	AI256147	ui95e12.x1 Sugano mouse liver mRNA Mus musculus cDNA clone IMAGE:1880190 3' mRNA sequence.	40,791	12-Nov-98
GB_BA1:CARCG12	2079	X14979	C. aurantiacus reaction center genes 1 and 2.	Chloroflexus aurantiacus	23-Apr-91
GB_BA1:SC7H2	42655	AL109732	Streptomyces coelicolor cosmid 7H2.	Streptomyces coelicolor A3(2)	2-Aug-99
GB_BA1:MTCY274	398991	Z74024	Mycobacterium tuberculosis H37Rv complete genome; segment 126/162.	Mycobacterium tuberculosis	19-Jun-98
GB_BA2:REU60056	2520	U60056	Ralstonia eutropha formate dehydrogenase-like protein (cbbBc) gene, complete cds. Ralstonia eutropha	Ralstonia eutropha	16-OCT-1996
rx00703	2409				
GB_GSS15:AQ604477	505	AQ604477	HS_2116_B1_G07 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2116 Col=13 Row=N, genomic survey sequence. zr14e07.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:6448804 3', mRNA sequence.	Homo sapiens	10-Jun-99
GB_EST11:AA224340	443	AA224340	yw7702:s1 Soares_placenta_8to9weeks_2NbHP8t09W Homo sapiens cDNA clone Homo sapiens IMAGE:258219 3', mRNA sequence.	Homo sapiens	35,129
GB_EST5:N30648	291	N30648	Mycobacterium tuberculosis H37Rv complete genome; segment 44/162. Mycobacterium leprae	Mycobacterium tuberculosis	11-MAR-1998
GB_BA1:MTCY10D7	39800	Z79700	Mycobacterium leprae cosmid L373.	Mycobacterium leprae	17-Jun-98
GB_BA1:MLC1373	37304	AL035500	Pseudomonas aeruginosa succinyl-CoA synthetase beta subunit (succC) and succinyl-Pseudomonas aeruginosa	Pseudomonas aeruginosa	27-Aug-99
GB_BA2:AF128399	2842	AF128399	CoA synthetase alpha subunit (sucD) genes, complete cds.		25-MAR-1999
rx00782	1005				
GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK42_F_20 map 17, *** SEQUENCING IN Homo sapiens PROGRESS *** , 14 unordered pieces.	Homo sapiens	28-Jul-98
GB_HTG2:AC008158	118792	AC008158	Homo sapiens chromosome 17 clone hRPK42_F_20 map 17, *** SEQUENCING IN Homo sapiens PROGRESS *** , 14 unordered pieces.	Homo sapiens	35,135
GB_PR3:AC005017	137176	AC005017	Homo sapiens BAC clone GS214N13 from 7p14-p15, complete sequence.	Homo sapiens	28-Jul-98
GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	8-Aug-98
GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	24-Jun-99
GB_PR2:HS151B14	128942	282188	Human DNA sequence from clone 151B14 on chromosome 22 Contains SOMATOSTATIN RECEPTOR TYPE 3 (SS3R) gene,pseudogene similar to ribosomal protein L39,RAC2 (RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 (P21-RAC2)) gene ESTs, STSS, GSSS and CpG islands, complete sequence.	Homo sapiens	27-Aug-99
rx00794	1128				
GB_BA1:HTG2:HSDJ319M7	616	AF016327	Hordeum vulgare Barperm1 (perm1) mRNA, partial cds.	Hordeum vulgare	30-Nov-99
GB_BA1:HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING Homo sapiens IN PROGRESS *** , in unordered pieces.	Homo sapiens	41,311
GB_BA1:HTG2:HSDJ319M7	128208	AL079341	Homo sapiens chromosome 6 clone RP1-319M7 map p21.1-21.3, *** SEQUENCING Homo sapiens IN PROGRESS *** , in unordered pieces.	Homo sapiens	36,845
rx00800	1227				
GB_BA1:MTV022	13025	AL021925	Mycobacterium tuberculosis H37Rv complete genome; segment 100/162.	Mycobacterium tuberculosis	30-Nov-99
GB_BA1:AB019513	4417	AB019513	Streptomyces coelicolor genes for alcohol dehydrogenase and ABC transporter, complete cds.	Streptomyces coelicolor	17-Jun-98
GB_PL1:SCSFAARP	7008	X68020	S.cerevisiae SFA and ARP genes.	S.cerevisiae cerevisiae	13-Nov-98
GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	29-Nov-94
GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	17-Jun-98
GB_BA2:AF169031	1141	AF169031	Xanthomonas oryzae pv. oryzae putative sugar nucleotide epimerase/dehydratase gene, partial cds.	Xanthomonas oryzae pv. oryzae	27-Aug-99
rx00871					14-Sep-99

**TABLE 4: ALIGNMENT RESULTS**

rx00872	1077	GB_IN1:CEF23H12	35564	274472	Caenorhabditis elegans cosmid F23H12, complete sequence.	<i>Caenorhabditis elegans</i>	34,502	08-OCT-1999		
		GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN Homo sapiens	Homo sapiens	35,714	24-MAY-1999		
		GB_HTG2:AC007263	167390	AC007263	Homo sapiens chromosome 14 clone BAC 79J20 map 14q31, *** SEQUENCING IN Homo sapiens	Homo sapiens	35,714	24-MAY-1999		
		GB_BA1:MTV049	40360	AL022021	Mycobacterium tuberculosis H37Rv complete genome; segment 81/162.	<i>Mycobacterium tuberculosis</i>	19-Jun-98			
		GB_PL2:CDU236897	1827	A1236897	<i>Candida dubliniensis</i> ACT1 gene, exons 1-2.	<i>Candida dubliniensis</i>	1-Sep-99			
		GB_PL1:CAACT1A	3206	X16377	<i>Candida albicans</i> act1 gene for actin.	<i>Candida albicans</i>	10-Apr-93			
		GB_BA2:AF010496	189370	AF010496	<i>Rhodobacter capsulatus</i> strain SB1003, partial genome.	<i>Rhodobacter capsulatus</i>	12-MAY-1998			
		GB_BA1:RMMPHA	7888	x93358	<i>Rhizobium meliloti</i> pha(A,B,C,D,E,F,G) genes.	<i>Rhizobium meliloti</i>	48,367	12-MAR-1999		
		GB_EST16C23528	317	C23528	C23528 Japanese flounder spleen <i>Paralichthys olivaceus</i> cDNA clone HB5(2), mRNA sequence.	<i>Paralichthys olivaceus</i>	41,640	28-Sep-99		
		rx00913	2118	GB_HTG2:AC007734	188267	AC007734	Homo sapiens chromosome 18 clone hRPK44_O_1 map 18, *** SEQUENCING IN Homo sapiens	34,457	5-Jun-98	
		GB_HTG2:AC007734	188267	AC007734	PRCGRESS ***, 18 unordered pieces.	PRCGRESS ***, 18 unordered pieces.				
		GB_EST18:AA709478	406	AA709478	Homo sapiens chromosome 18 clone hRPK44_O_1 map 18, *** SEQUENCING IN Homo sapiens	Homo sapiens	34,457	5-Jun-98		
		GB_EST18:AA709478	406	AA709478	PRCGRESS ***, 18 unordered pieces.	PRCGRESS ***, 18 unordered pieces.				
		rx00945	1095	GB_HTG4:AC010351	220710	AC010351	w3ta5,r1 Striagene mouse heart #937316) <i>Mus musculus</i> cDNA clone	<i>Mus musculus</i>	42,065	24-DEC-1997
		GB_HTG4:AC010351	220710	AC010351	IMAGE:1224275, mRNA sequence.					
		GB_HTG4:AC010351	220710	AC010351	Homo sapiens chromosome 5 clone C1TB-H1_2022B6, *** SEQUENCING IN	Homo sapiens	36,448	31-OCT-1999		
		GB_BA1:MTCY05A6	38631	Z96072	PROGRESS ***, 68 unordered pieces.	Homo sapiens	36,448	31-OCT-1999		
		GB_BA1:MTCY05A6	38631	Z96072	Homo sapiens chromosome 5 clone C1TB-H1_2022B6, *** SEQUENCING IN	Homo sapiens	36,218	17-Jun-98		
		rx00965			PROGRESS ***, 68 unordered pieces.	<i>Mycobacterium tuberculosis</i>				
		rx00999	1575	GB_PAT:E13660	1916	E13660	gDNA encoding 6-phosphogluconate dehydrogenase.	Cornebacterium glutamicum	98,349	24-Jun-98
		GB_BA1:MTCY359	36021	Z83859	<i>Mycobacterium tuberculosis</i> H37Rv complete genome; segment 84/162.	<i>Mycobacterium tuberculosis</i>	38,520	17-Jun-98		
		GB_BA1:MLCB1788	39228	AL008609	<i>Mycobacterium leprae</i> cosmid B1788.	<i>Mycobacterium leprae</i>	64,355	27-Aug-99		
		GB_BA1:MTV008	63033	AL021246	<i>Mycobacterium tuberculosis</i> H37Rv complete genome; segment 108/162.	<i>Mycobacterium tuberculosis</i>	39,860	17-Jun-98		
		GB_BA1:MTV008	63033	AL021246	<i>Mycobacterium tuberculosis</i> H37Rv complete genome; segment 108/162.	<i>Mycobacterium tuberculosis</i>	39,120	17-Jun-98		
		rx01025	1119	GB_BA1:SC7A1	32039	AL034447	Streptomyces coelicolor cosmid TA1.	Streptomyces coelicolor	55,287	15-DEC-1998
		GB_BA1:MSGBI723CS	38477	L78825	<i>Mycobacterium leprae</i> cosmid B1723 DNA sequence.	<i>Mycobacterium leprae</i>	56,847	15-Jun-96		
		GB_BA1:MLCB337	44982	Z98263	<i>Mycobacterium leprae</i> cosmid B837.	<i>Mycobacterium leprae</i>	56,676	17-Sep-97		
		GB_BA2:AF017444	3067	AF017444	<i>Sinorhizobium meliloti</i> NADP-dependent malic enzyme (lme) gene, complete cds.	<i>Sinorhizobium meliloti</i>	53,660	2-Nov-97		
		GB_BA1:BSUB0013	216470	Z99116	Bacillus subtilis complete genome (section 13 of 21); from 2395261 to 2613730.	<i>Bacillus subtilis</i>	37,255	26-Nov-97		
		GB_VI:HSV2HG52	154746	Z86099	Herpes simplex virus type 2 (strain HG52), complete genome.	Human herpesvirus 2	38,081	04-DEC-1998		
		GB_HTG2:AC002518	131855	AC002518	***, 11 unordered pieces.	Homo sapiens	35,647	2-Sep-97		
		GB_HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS	Homo sapiens	35,647	2-Sep-97		
					***, 11 unordered pieces.					

**TABLE 4: ALIGNMENT RESULTS**

GB-HTG2:AC002518	131855	AC002518	Homo sapiens chromosome X clone bWXD20, *** SEQUENCING IN PROGRESS	Homo sapiens	26,180	2-Sep-97	
***, 11 unordered pieces.							
rx01077 1494	GB_PR3:HSDJ653C5	85237	AL049743	Human DNA sequence from clone 663C5 on chromosome 1p21.3-22.3 Contains CA Homo sapiens repeat(D1S435), STRs and GSSs, complete sequence.	36,462	23-Nov-99	
GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	41,808	1-Jul-95	
GB_BA1:ECU29579	72221	U29579	Escherichia coli K-12 genome; approximately 61 to 62 minutes.	Escherichia coli	36,130	1-Jul-95	
GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18-TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	36,528	14-Jul-98	
GB_GSS8:AQ042907	392	AQ042907	CIT-HSP-2318D17-TR CIT-HSP Homo sapiens genomic clone 2318D17, genomic survey sequence.	Homo sapiens	35,969	14-Jul-98	
GB_GSS8:AQ044021	387	AQ044021	CIT-HSP-2318C18-TR CIT-HSP Homo sapiens genomic clone 2318C18, genomic survey sequence.	Homo sapiens	44,545	14-Jul-98	
rx01093 1554	GB_BA1:CORPYK1	2795	L27126	Corynebacterium pyruvate kinase gene, complete cds.	Corynebacterium glutamicum	100,000	07-DEC-1994
GB_BA1:MTCY01B2	35938	Z99554	Mycobacterium tuberculosis H37Rv complete genome, segment 72/162.	Mycobacterium tuberculosis	63,771	17-Jun-98	
GB_BA1:MIU65430	1439	U65430	Mycobacterium intracellulare pyruvate kinase (pykF) gene, complete cds.	Mycobacterium intracellulare	67,061	23-DEC-1996	
GB_BA2:AF045998	780	AF045998	Corynebacterium glutamicum inositol monophosphate phosphatase (impA) gene, complete cds.	Corynebacterium glutamicum	99,615	19-Feb-98	
GB_BA2:AF051846	738	AF051846	Corynebacterium glutamicum phosphoribosylformimino-5-amino-1-phosphoribosyl-4-Corynebacterium glutamicum imidazolecarboxamide isomerase (hisA) gene, complete cds.	Corynebacterium glutamicum	100,000	12-MAR-1998	
GB_GSS1:FR0005503	619	289313	F.rubripes GSS sequence, clone 079B16aE8, genomic survey sequence.	F.rubripes	37,785	01-MAR-1997	
GB_PR3:AC004063	177014	AC004063	Homo sapiens chromosome 4 clone B3218, complete sequence.	Homo sapiens	35,835	10-Jul-98	
GB_PR3:HS1178121	62268	AL109852	Human DNA sequence from clone RP5-1178121 on chromosome X, complete sequence.	Homo sapiens	37,873	01-DEC-1999	
GB-HTG3:AC009301	163369	AC009301	Homo sapiens clone NH0062F14, *** SEQUENCING IN PROGRESS *** , 5 unordered pieces.	Homo sapiens	37,240	13-Aug-99	
GB-HTG3:AC009444	164587	AC009444	Homo sapiens clone 1_O_3, *** SEQUENCING IN PROGRESS *** , 8 unordered pieces.	Homo sapiens	38,416	22-Aug-99	
GB-HTG3:AC009444	164587	AC009444	Drosophila melanogaster cosmid 66A1.	Drosophila melanogaster	38,416	22-Aug-99	
GB_IN1:DMC66A1	34127	AL031227	C(glutamicum (ASO 19) ATPase beta-subunit gene.	Corynebacterium glutamicum	99,931	05-OCT-1998	
GB_BA1:CGASO19	1452	X76875	Brevibacterium flavum UncD gene whose gene product is involved in Hepatitis C virus	Corynebacterium glutamicum	99,242	27-OCT-1994	
EM_PAT:EP09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in Hepatitis C virus	(Rei. 32, Created)	07-OCT-1997	07-OCT-1997 (Rei. 32, Created)	
GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	39,153	09-MAR-1995	
EM_PAT:EP09634	1452	E09634	Brevibacterium flavum UncD gene whose gene product is involved in Hepatitis C virus	Corynebacterium glutamicum	100,000	07-OCT-1997	
GB_BA1:CGASO19	1452	X76875	S.lividans l protein and ATP synthase genes.	Corynebacterium glutamicum	100,000	27-OCT-1994	
GB_VI:HECRE4B	414	X60570	C(glutamicum (ASO 19) ATPase beta-subunit gene.	Hepatitis C virus	36,769	5-Apr-92	
rx011200			Hepatitis C genomic RNA for putative envelope protein (RE4B isolate).				
rx01194 495	GB_BA1:SLATPSYNA	8560	Z22606	S.lividans l protein and ATP synthase genes.	Streptomyces lividans	66,269	01-MAY-1995
	GB_BA1:MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162.	Mycobacterium tuberculosis	65,437	17-Jun-98

**TABLE 4: ALIGNMENT RESULTS**

rx01202 1098	GB_BA1:MLU15186 GB_BA1:SLATPSYNA GB_BA1:SLATPSYNA GB_BA1:MCSSQSSH GB_PL1:AP000423	36241 8560 8560 5538 154478	U15186 Z22606 Z22606 Y09978 AP000423	Mycobacterium leprae cosmid L471. <i>S.lividans</i> i protein and ATP synthase genes. <i>S.lividans</i> i protein and ATP synthase genes. <i>M.capsulatus</i> orfx, orfy, orfz, sqs and shc genes. <i>Arabidopsis</i> thaliana chloroplast genomic DNA, complete sequence, strain:Columbia. <i>Chloroplast Arabidopsis thaliana</i>	39,302 57,087 38,298 37,626 38,395	09-MAR-1995 01-MAY-1995 01-MAY-1995 26-MAY-1998 15-Sep-99
GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114116, *** SEQUENCING IN PROGRESS *** , 39	Homo sapiens	35,459	04-DEC-1999
GB_HTG6:AC009762	164070	AC009762	Homo sapiens clone RP11-114116, *** SEQUENCING IN PROGRESS *** , 39	Homo sapiens	36,117	04-DEC-1999
rx01216 1124	GB_BA1:MTCY10G2 GB_BA2:AF017435	38970 4301	Z92539 AF017435	Mycobacterium tuberculosis H37Rv complete genome; segment 47/162. <i>Methylobacterium extorquens</i> methanol oxidation genes, glmU-like gene, partial cds, <i>Methylobacterium extorquens</i> and orfL2, orfL1, orfR genes, complete cds.	39,064 42,671	17-Jun-98 10-MAR-1998
rx01225 1563	GB_BA1:CCRELBDBA GB_BA2:AF058302	4424 23306	M69228 AF058302	<i>Candidatus crescentus</i> C.crescentus flagellar gene promoter region. <i>Streptomyces roseofulvus</i> frenolicin biosynthetic gene cluster, complete sequence.	41,054 36,205	26-Apr-98 2-Jun-98
GB_HTG3:AC007301	165741	AC007301	Drosophila melanogaster chromosome 2 clone BAC04B09 (D576) RPCI-98 04.B.9 Drosophila melanogaster map 43E12-44F1 strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 150	Drosophila melanogaster chromosome 2 clone BAC04B09 (D576) RPCI-98 04.B.9 Drosophila melanogaster map 43E12-44F1 strain y; cn bw sp, *** SEQUENCING IN PROGRESS *** , 150	39,922	17-Aug-99
rx01227 444	GB_BA1:SERFDXA GB_BA1:MTV005 GB_BA1:MSGY348 GB_PR3:AC005697	3669 37840 40056 174503	M61119 AL010186 AD000020 AC005697	<i>Saccharopolyspora erythraea</i> ferredoxin (fdxa) gene, complete cds. Mycobacterium tuberculosis H37Rv complete genome; segment 51/162. <i>Mycobacterium tuberculosis</i> sequence from clone y348. <i>Homo sapiens</i> chromosome 17, clone hRPK138_P_22, complete sequence.	64,908 62,838 61,712 35,373	13-MAR-1996 17-Jun-98 10-DEC-1996 09-OCT-1998
rx01242 900	GB_HTG3:AC010722	160723	AC010722	<i>Homo sapiens</i> clone NH0122L09, *** SEQUENCING IN PROGRESS *** , 2 unordered pieces.	39,863	25-Sep-99
GB_HTG3:AC010722	160723	AC010722	<i>Homo sapiens</i> clone NH0122L09, *** SEQUENCING IN PROGRESS *** , 2 unordered pieces.	<i>Homo sapiens</i>	39,863	25-Sep-99
rx01243 1083	GB_GSS10:AQ255057	583	AQ255057	mgb0008N01r CUG Rice Blast BAC Library Magnaporthe grisea genomic clone mgb0008N01r, genomic survey sequence.	38,722	23-OCT-1998
GB_IN1:CEK05D4 GB_IN1:CEK05D4	19000 19000	292804 292804	Caenorhabditis elegans cosmid K05D4, complete sequence. Caenorhabditis elegans cosmid K05D4, complete sequence.	Caenorhabditis elegans Caenorhabditis elegans	35,448 35,694	23-Nov-98 23-Nov-98
GB_BA1:GLPD GB_HTG4:AC010567	1800 143287	Y16642 AC010567	<i>Corynebacterium glutamicum</i> lpd gene, complete CDS. <i>Drosophila melanogaster</i> chromosome 3L/69C1 clone RPCI98-11N6, *** SEQUENCING IN PROGRESS *** , 70 unordered pieces.	<i>Corynebacterium glutamicum</i> <i>Drosophila melanogaster</i>	100,000 37,178	1-Feb-99 16-OCT-1999
GB_HTG4:AC010567	143287	AC010567	<i>Drosophila melanogaster</i> chromosome 3L/69C1 clone RPCI98-11N6, *** SEQUENCING IN PROGRESS *** , 70 unordered pieces.	<i>Drosophila melanogaster</i>	37,178	16-OCT-1999
rx01262 1284	GB_BA2:AF172324	14263	AF172324	Escherichia coli GalF (galF) gene, partial cds; O-antigen repeat unit transporter Wzx Escherichia coli (wzx), WbnA (wbnA), O-antigen polymerase Wzy (wzy), WbnB (wbnB), WbnC (wbnC), WbnD (wbnD), WbnE (wbnE), UDP-Glc-4-epimerase GalE (galE), 6-phosphogluconate dehydrogenase Gnd (gnd), UDP-Glc-6-dehydrogenase Ugd (ugd), and WbnF (wbnF) genes, complete cds; and chain length determinant Wzz (wzz) gene, partial cds.	59,719	29-OCT-1999

**TABLE 4: ALIGNMENT RESULTS**

	GB_BA2:ECU78086	4759	U78086	Escherichia coli hypothetical uridine-5'-diphosphoglucose dehydrogenase (ugd) and Escherichia coli O-chain length regulator (wzz) genes, complete cds.	59,735	5-Nov-97
rx01311 870	GB_BA1:D90841 GB_PR3:AC004103	20226 144368	D90841 AC004103	E.coli genomic DNA, Kohara clone #51145(1-45.5 min.). Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.	37,904 37,340	21-MAR-1997 18-Apr-98
GB_HTG3:AC007383		215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	36,385	25-Sep-99
GB_HTG3:AC007383		215529	AC007383	Homo sapiens clone NH0310K15, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	36,385	25-Sep-99
rx01312 2142	GB_BA2:AE000487 GB_BA1:MTV016 GB_BA1:U00022 GB_HTG4:AC009245	13889 53662 36411 215767	AE000487 AL021841 U00022 AC009245	Escherichia coli K-12 MG1655 section 377 of 400 of the complete genome. Mycobacterium tuberculosis H37Rv complete genome; segment 143/162. Mycobacterium leprae cosmid L308. Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered Homo sapiens pieces.	39,494 46,252 46,368 36,016	12-Nov-98 23-Jun-99 01-MAR-1994 2-Nov-99
GB_HTG4:AC009245		215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered Homo sapiens pieces.	36,016	2-Nov-99
GB_HTG4:AC009245		215767	AC009245	Homo sapiens chromosome 7, *** SEQUENCING IN PROGRESS ***, 24 unordered Homo sapiens pieces.	39,618	2-Nov-99
rx01325 795	GB_HTG6:AC007186	225851	AC007186	Drosophila melanogaster chromosome 2 clone BACR03D06 (D569) RPCI-98 03.D.6 Drosophila melanogaster map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 91 unordered pieces.	35,366	07-DEC-1999
GB_HTG6:AC007147		202291	AC007147	Drosophila melanogaster chromosome 2 clone BACR19N18 (D572) RPCI-98 19.N.18 map 32A-32A strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 22 unordered pieces.	35,366	07-DEC-1999
GB_HTG3:AC010207		207890	AC010207	Homo sapiens clone RPC11-375120, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.	34,821	16-Sep-99
rx01350 1107	GB_BA2:AF109682 GB_HTG2:AC006759	990 103725	AF109682 AC006759	Aquaspirillum arcticum malate dehydrogenase (MDH) gene, complete cds. Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS ***, 8 Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS ***, 8 Caenorhabditis elegans clone Y40G12, *** SEQUENCING IN PROGRESS ***, 8 Caenorhabditis elegans	58,487 37,963 37,963 37,963	19-OCT-1999 25-Feb-99 25-Feb-99 25-Feb-99
GB_HTG2:AC006759		103725	AC006759	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162. Xanthomonas campestris phosphoglucomutase and phosphomannomutase (xanA) and phosphomanno isomerase and GDP-mannose pyrophosphorylase (xanB) genes, complete cds.	38,011 47,726	17-Jun-98 26-Apr-93
rx01365 1497	GB_BA1:MTY20B11 GB_BA1:XANXANAB	36330 3410	Z95121 M83231	RPC11-47D24.T7 RPCI-11 Homo sapiens genomic clone T21A19, genomic survey sequence.	36,599	20-Apr-99
GB_GSS10:AQ194038		697	AC194038	Mycobacterium tuberculosis H37Rv complete genome; segment 139/162. Arabidopsis thaliana genomic clone T27A19, genomic survey sequence.	36,940 35,284	17-Jun-98 14-MAY-1997
rx01369 1305	GB_BA1:MTY20B11 GB_GSS3:BI0037	36330 974	Z95121 B10037	T21A19-T7.1 TAMU Arabidopsis thaliana genomic clone T21A19, genomic survey sequence.	38,324	14-MAY-1997
GB_GSS3:BI00549		1097	B09549	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162. Arabidopsis thaliana	39,778 32,658	10-Feb-99 16-Nov-99
rx01377 1209	GB_BA1:MTCY71 GB_HTG5:AC007547	42729 262181	Z92771 AC007547	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162. Homo sapiens clone RP11-252018, WORKING DRAFT SEQUENCE, 121 unordered pieces.		

**TABLE 4: ALIGNMENT RESULTS**

				Homo sapiens			
GB-HTG5:AC007547	262181	AC007547	Homo sapiens clone RP11-252O18, WORKING DRAFT SEQUENCE, 121 unordered pieces.		38,395	16-Nov-99	
rx01392 1200	GB_BA2:AF072709	8366	AF072709	Streptomyces lividans amplifiable element AUD4; putative regulator, putative ferredoxin, putative cytochrome putative oxidoreductase genes, complete cds; and unknown genes.	55,221	8-Jul-98	
GB_BA1:CGLYSEG GB_PRA4:AC005906	2374	X96471	X89084	P450 oxidoreductase, and C:glutamicum lysE and lvsG genes.	24-Feb-97		
GB_BA1:CGPTAAACKA GB_BA1:D08861	14839	D9861	Homo sapiens 12p13.3 BAC RPC11-429A20 (Roswell Park Cancer Human BAC Library) complete sequence.	Institute Homo sapiens	36,756	30-Jan-99	
GB_PATI:ED2087	1200	E02087	C:glutamicum pta gene and ackA gene. E.coli genomic DNA, Kohara clone #405(52.0-52.3 min.).	Corynebacterium glutamicum	100,000	23-MAR-1999	
GB_GSS1:HPU60627	280	U60627	DNA encoding acetate kinase protein from Escherichia coli.	Escherichia coli	63,041	29-MAY-1997	
GB_EST31:AI701691	349	A1701691	Helicobacter pylori feoB-like DNA sequence, genomic survey sequence. we81c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347494 3' similar to gb:L19886_mna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN); mRNA sequence.	Helicobacter pylori	54,461	29-Sep-97	
GB_EST15:AA480256	389	AA480256	ne3/f04.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:898975_3' similar to Homo sapiens gb:L19886_mna1 MACROPHAGE MIGRATION INHIBITORY FACTOR (HUMAN); mRNA sequence.	Homo sapiens	39,286	9-Apr-97	
rx01478 1959	GB_BA1:SCI51 GB_BA1:SCE36 GB_BA1:CGU3535	40745 12581 2531	AL109848 AL049763 U45355	Streptomyces coelicolor cosmid 151. Streptomyces coelicolor cosmid E36. Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds, Corynebacterium glutamicum mRNA sequence.	Streptomyces coelicolor A3(2) Streptomyces coelicolor Corynebacterium glutamicum	54,141 38,126 41,852	16-Aug-99 05-MAY-1999 9-Apr-97
rx01482 1998	GB_BA1:SC6G4 GB_BA1:J00020 GB_BA1:MTCY77	41055 36947 22255	AL031317 U00020 Z93389	Streptomyces coelicolor cosmid 6G4. Mycobacterium leprae cosmid B229. Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Streptomyces coelicolor Mycobacterium leprae Mycobacterium tuberculosis	62,149 38,303 38,179	20-Aug-98 01-MAR-1994 18-Jun-98
rx01534							
rx01535 1530	GB_BA1:MLCB1222 GB_BA1:MTV017 GB_BA1:PAU72494	34714 67200 43686	AL049491 AL021897 U72494	Mycobacterium leprae cosmid B1222. Mycobacterium tuberculosis H37Rv complete genome; segment 48/162. Pseudomonas aeruginosa fumarase (fumC) and Mn superoxide dismutase (sodA) genes, complete cds.	Mycobacterium leprae Mycobacterium tuberculosis Pseudomonas aeruginosa	66,208 38,553 52,690	27-Aug-99 24-Jun-99 23-OCT-1996
rx01550 1635	GB_BA1:D90907 GB_IN2:AF073177 GB_IN2:AF073179	132419 9534 3159	D90907 AF073177 AF073179	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885. Drosophila melanogaster glycogen phosphorylase (GlyP) gene, complete cds. Drosophila melanogaster glycogen phosphorylase (Glp1) mRNA, complete cds.	Synechocystis sp. Drosophila melanogaster Drosophila melanogaster	56,487 55,100 56,708	7-Feb-99 1-Jul-99 27-Apr-99
rx01562							
rx01569 1482	GB_BA1:D78182	7836	D78182	Streptococcus mutans DNA for dTDP-rihamnoside synthesis pathway, complete cds.	Streptococcus mutans	44,050	5-Feb-99
GB_BA2:AF079139 GB_BA2:AF087022	4342 1470	AF079139 AF087022	Streptomyces venezuelae pikCD operon, complete sequence. Streptomyces venezuelae cytochrome P450 monooxygenase (pikC) gene, complete cds.	Streptomyces venezuelae Streptomyces venezuelae	38,587 38,621	28-OCT-1998 15-OCT-1998	
rx01570 978	GB_BA1:MTCY63	38900	Z96800	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	Mycobacterium tuberculosis	59,035	17-Jun-98

**TABLE 4: ALIGNMENT RESULTS**

GB_BA2:AF097519	4594	AF097519	Klebsiella pneumoniae dTDP-D-glucose 4,6 dehydratase (rmlB), glucose-1-phosphate thymidyl transferase (rmlA), dTDP-4-keto-L-rhamnose reductase (rmlD), dTDP-4-keto-6-deoxy-D-glucose 3,5-epimerase (rmlC), and rhamnosyl transferase (wblB) genes, complete cds.	<i>Klebsiella pneumoniae</i>	59,714	4-Nov-98	
GB_BA2:NGOCPSPS	8905	L09189	<i>Neisseria meningitidis</i> dTDP-D-glucose 4,6-dehydratase (rnb), glucose-1-phosphoryl transferase (rnbA) and rfbC genes, complete cds and UDP-glucosidase (galE) pseudogene.	<i>Streptomyces griseus</i>	58,384	30-Jul-98	
rx01571 723	GB_BA1:AB011413	12070	AB011413	<i>Streptomyces griseus</i> genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	<i>Streptomyces griseus</i>	57,500	7-Aug-98
GB_BA1:AB011413	12070	AB011413	<i>Streptomyces griseus</i> genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	<i>Streptomyces griseus</i>	35,655	7-Aug-98	
rx01572 615	GB_BA1:AB011413	12070	AB011413	<i>Streptomyces griseus</i> genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	<i>Streptomyces griseus</i>	57,843	7-Aug-98
GB_BA1:AB011413	12070	AB011413	<i>Streptomyces griseus</i> genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.	<i>Streptomyces griseus</i>	38,119	7-Aug-98	
rx01606 2799	GB_VtCFU72240	4783	U72240	<i>Choristoneura fumiferana</i> nuclear polyhedrosis virus ETM protein homolog, 79 kDa nucleopolyhedrovirus protein homolog, 15 kDa protein homolog and GTA protein homolog genes, complete cds.	<i>Choristoneura fumiferana</i> nucleopolyhedrovirus	37,115	29-Jan-98
GB_GSS10:AQ213248	408	AQ213248	HS_3249_B1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3249 Col=3 Row=B, genomic survey sequence.	Homo sapiens	34,559	18-Sep-98	
GB_GSS8:AQ070145	285	AQ070145	HS_3027_B1_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=P, genomic survey sequence.	Homo sapiens	40,351	5-Aug-98	
rx01626 468	GB_PR4:AF152510	2490	AF152510	Homo sapiens protocadherin gamma A3 short form protein (PCDH-gamma-A3) variable region sequence, complete cds.	Homo sapiens	34,298	14-Jul-99
GB_PR4:AF152323	4605	AF152323	Homo sapiens protocadherin gamma A3 (PCDH-gamma-A3) mRNA, complete cds.	Homo sapiens	34,298	22-Jul-99	
GB_PR4:AF152509	2712	AF152509	Homo sapiens PCDH-gamma-A3 gene, aberrantly spliced, mRNA sequence.	Homo sapiens	34,298	14-Jul-99	
GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13 N.2 Drosophila melanogaster map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999	
GB_HTG4:AC006590	127171	AC006590	Drosophila melanogaster chromosome 2 clone BACR13N02 (D543) RPCI-98 13.N.2 Drosophila melanogaster map 36E-36E strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 101 unordered pieces.	Drosophila melanogaster	33,812	19-OCT-1999	
GB_GSS8:B99182	415	B99182	CIT-HSP-228013.TR CIT-HSP Homo sapiens genomic clone 2280113, genomic survey sequence.	Homo sapiens	36,111	26-Jun-98	
GB_BA1:BSUB0009	208780	Z99112	<i>Bacillus subtilis</i> complete genome (section 9 of 21): from 1598421 to 1807200.	<i>Bacillus subtilis</i>	36,591	26-Nov-97	
GB_BA1:BSUB0009	208780	Z99112	<i>Bacillus subtilis</i> complete genome (section 9 of 21): from 1598421 to 1807200.	<i>Bacillus subtilis</i>	36,591	26-Nov-97	
GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48110 (D505) RPCI-98 48.1.10 Drosophila melanogaster map 49E6-49F8 strain y; cn bw sp, *** SEQUENCING IN PROGRESS **, 17 unordered pieces.	Drosophila melanogaster	37,037	2-Aug-99	
rx01695 1623	GB_BA1:CGA224946	2408	AJ224946	<i>Corynebacterium glutamicum</i> DNA for L-Malate:quinone oxidoreductase.	<i>Corynebacterium glutamicum</i>	100,000	11-Aug-98
GB_BA1:MTCY24A1	20270	Z95207	Mycobacterium tuberculosis H37Rv complete genome; segment 124/162.	<i>Mycobacterium tuberculosis</i>	38,626	17-Jun-98	
GB_JN1:DMU15974	2994	U15974	Drosophila melanogaster kinesin-like protein (Klp68d) mRNA, complete cds.	<i>Drosophila melanogaster</i>	36,783	18-Jul-95	

**TABLE 4: ALIGNMENT RESULTS**

rx01702	1155	GB_BA1:CGFDA	3371	X17313	Corynebacterium glutamicum fda gene for fructose-bisphosphate aldolase (EC 4.1.2.13).	Corynebacterium glutamicum	99,913	12-Sep-93
		GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	38,786	17-Jun-98
		GB_BA1:MLCB4	36310	AL025514	Mycobacterium leprae cosmid B4.	Mycobacterium leprae	38,238	27-Aug-98
		GB_IN2:CELC27H5	35840	U14635	Caenorhabditis elegans cosmid C27H5.	Caenorhabditis elegans	35,334	13-Jul-95
		GB_EST24:AI167112	579	AI167112	xylem.est:878 Poplar xylem Lambda ZAPI library Populus balsamifera subsp. trichocarpa cDNA 5', mRNA sequence.	Populus balsamifera subsp. trichocarpa	39,222	03-DEC-1998
		GB_GSS9:AQ102635.	347	AQ102635	HS_3048_B1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=15 Row=L, genomic survey sequence.	Homo sapiens	40,653	27-Aug-98
		GB_BA1:MTCY01B2	35938	Z95554	Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.	Mycobacterium tuberculosis	36,650	17-Jun-98
		GB_GSS1:AF009226	665	AF009226	Mycobacterium tuberculosis cytochrome D oxidase subunit I (appC) gene, partial sequence. genomic survey sequence.	Mycobacterium tuberculosis	63,438	31-Jul-97
		GB_BA1:SCD78	36224	AL034355	Streptomyces coelicolor cosmid D78.	Streptomyces coelicolor	53,088	26-Nov-98
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	62,081	17-Jun-98
		GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	61,364	22-Aug-97
		GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	52,323	12-Nov-98
		GB_PR3:HS57G9	113872	Z95116	Human DNA sequence from BAC 57G9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.	Homo sapiens	39,209	23-Nov-98
		GB_PL2:YSCH9666	39057	U10397	Saccharomyces cerevisiae chromosome VII cosmid 9666.	Saccharomyces cerevisiae	40,021	5-Sep-97
		GB_PL2:YSCH9986	41664	U00027	Saccharomyces cerevisiae chromosome VIII cosmid 9986.	Saccharomyces cerevisiae	34,375	29-Aug-97
		GB_BA1:ABCCELB	2058	L24077	Acetobacter xylinum phosphoglucomutase (celB) gene, complete cds.	Acetobacter xylinum	62,173	21-Sep-94
		GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	39,749	17-Jun-98
		GB_BA1:MTCY22D7	31859	Z83866	Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.	Mycobacterium tuberculosis	40,034	17-Jun-98
		GB_GSS9:AQ142579	529	AQ142579	HS_2222_B1_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=5 Row=P, genomic survey sequence.	Homo sapiens	38,068	24-Sep-98
		GB_IN2:AC005889	108924	AC005889	Drosophila melanogaster, chromosome 2L, region 30A3-30A6, P1 clones DS06958 and DS03097, complete sequence.	Drosophila melanogaster	36,557	30-OCT-1998
		GB_GSS1:AG008814	637	AG008814	Homo sapiens genomic DNA, 21q region, clone: B137B7BB68, genomic survey sequence.	Homo sapiens	35,316	7-Feb-99
		GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnal) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,364	03-OCT-1999
		GB_HTG5:AC008031	158889	AC008031	Trypanosoma brucei chromosome II clone RPCI93-25N14, *** SEQUENCING IN PROGRESS *** 2 unordered pieces.	Trypanosoma brucei	35,334	15-Nov-99
		GB_BA2:AF183408	63626	AF183408	Microcystis aeruginosa DNA polymerase III beta subunit (dnal) gene, partial cds; microcystin synthetase gene cluster, complete sequence; Uma1 (uma1), Uma2 (uma2), Uma3 (uma3), Uma4 (uma4), and Uma5 (uma5) genes, complete cds; and Uma6 (uma6) gene, partial cds.	Microcystis aeruginosa	36,529	03-OCT-1999
		GB_BA1:SERFDXA	3869	M61119	Saccharopolyspora erythraea ferredoxin (fdxA) gene, complete cds.	Saccharopolyspora erythraea	59,862	13-MAR-1996
		GB_BA1:MTV005	37840	AL010186	Mycobacterium tuberculosis H37Rv complete genome; segment 51/162.	Mycobacterium tuberculosis	61,949	17-Jun-98
		GB_BA1:MSGY348	40056	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	59,908	10-DEC-1996
		GB_PR1:HUMADRA2C	1491	J03853	Human kidney alpha-2-adrenergic receptor mRNA, complete cds.	Homo sapiens	36,989	27-Apr-93
		GB_PR4:HSU72648	4850	U72648	Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds.	Homo sapiens	36,989	23-Nov-98

TABLE 4: ALIGNMENT RESULTS

GB_GSS3:BA42200	387	B42200	HS-1055-B1-A03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=5 Row=B, genomic survey sequence.	Homo sapiens	34,805	18-OCT-1997	
rx01884 1913	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	37,892	17-Jun-98
	GB_BA1:SCO001206	9184	AJ001206	Streptomyces coelicolor A3(2), glycogen metabolism cluster II.	Streptomyces coelicolor	40,413	29-MAR-1999
	GB_BA1:D90908	122349	D90908	Synechocystis sp. PCC6803 complete genome, 10/27, 118886-1311234.	Synechocystis sp.	47,792	7-Feb-99
rx01886 897	GB_GSS9:AAQ116291	572	AQ116291	RPC11-49P6.TK_1 RPC1-11 Homo sapiens genomic clone RPC1-11-49P6, genomic survey sequence.	Homo sapiens	43,231	20-Apr-99
	GB_BA2:AE001721	17632	AE001721	Thermotoga maritima section 33 of 136 of the complete genome.	Thermotoga maritima	39,306	2-Jun-99
	GB_EST16:AA567090	596	AA567090	GM01044 5prime GM Drosophila melanogaster ovary BlueScript Drosophila melanogaster cDNA clone GM01044 5prime, mRNA sequence.	Drosophila melanogaster	42,807	28-Nov-98
rx01887 1134	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***, 102	Homo sapiens	36,417	03-DEC-1999
	GB_HTG6:AC008147	303147	AC008147	Homo sapiens clone RP3-405J10, *** SEQUENCING IN PROGRESS ***, 102	Homo sapiens	37,687	03-DEC-1999
	GB_BA2:ALLW243431	26953	AJ243431	Acinetobacter lwoffii wzc, wzb, weeB, weeC, wzx, wzY, weeD, weeE, weeF, weeG, weeH, weeI, weeL, weeT, galU, ugd, pgI, galE, pgM (partial) and mfp (partial) genes (emulsion biosynthetic gene cluster), strain RAG-1.	Acinetobacter lwoffii	39,640	01-OCT-1999
rx01888 658	GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPC-98 02.L.12 Drosophila melanogaster map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 113	Drosophila melanogaster	32,969	2-Aug-99
	GB_HTG2:AC008197	125235	AC008197	Drosophila melanogaster chromosome 3 clone BACR02L12 (D753) RPC-98 02.L.12 Drosophila melanogaster map 94B-94C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 113	Drosophila melanogaster	32,969	2-Aug-99
	GB_EST36:AI881527	598	AI881527	606070C09.y1 606 - Ear tissue cDNA library from Schmidt lab Zea mays cDNA, mRNA sequence.	Zea mays	43,617	21-Jul-99
rx01891 887	GB_Vi:HIV232971	621	AJ232971	Human immunodeficiency virus type 1 subtype C nef gene, patient MP83.	Human immunodeficiency virus type 1	40,040	05-MAR-1999
	GB_PL1:AFCHSE	6158	Y09542	A.fumigatus chsE gene.	Aspergillus fumigatus	37,844	1-Apr-97
	GB_PR3:AF064858	193387	AF064858	Homo sapiens chromosome 21q22.3 BAC 28F9, complete sequence.	Homo sapiens	37,136	2-Jun-98
rx01895 1051	GB_BA1:CGSL238250	1593	AJ238250	Corynebacterium glutamicum nth gene.	Corynebacterium glutamicum	100,000	24-Apr-99
	GB_BA2:AF038423	1376	AF038423	Mycobacterium smegmatis NADH dehydrogenase (ndh) gene, complete cds.	Mycobacterium smegmatis	65,254	05-MAY-1998
	GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	40,058	17-Jun-98
rx01901 1383	GB_BA1:MSGB38COS	37114	L01095	M. leprae genomic DNA sequence, cosmid B38 bfr gene, complete cds.	Mycobacterium leprae	59,551	6-Sep-94
	GB_BA1:SCE63	37200	AL035840	Streptomyces coelicolor cosmid E63.	Streptomyces coelicolor	38,468	17-MAR-1999
	GB_PR3:AF093117	147216	AF093117	Homo sapiens chromosome 7q10 BAC E3, complete sequence.	Homo sapiens	39,291	02-OCT-1998
rx01927 1503	GB_BA1:CGPAN	2164	X96580	C.glutamicum panB, panC & xylB genes.	Corynebacterium glutamicum	38,384	11-MAY-1999
	GB_BA1:ASXYLA	1905	X59466	Arthrobacter Sp. N.R.R.L. B3728 xyA gene for D-xylene(D-glucose) Isomerase.	Arthrobacter sp.	56,283	04-MAY-1992
	GB_HTG3:AC009500	176060	AC009500	Homo sapiens clone NH0511A20, *** SEQUENCING IN PROGRESS ***, 6	Homo sapiens	37,593	24-Aug-99
				unordered pieces.			
rx01952 1836	GB_BA2:AE000739	13335	AE000739	Aquifex aeolicus section 71 of 109 of the complete genome.	Aquifex aeolicus	36,309	25-MAR-1998
	GB_EST28:AI519629	612	AI519629	LD3282.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD3282 5prime, mRNA sequence.	Drosophila melanogaster	41,941	16-MAR-1999
	GB_EST21:AA949396	767	AA949396	LD2227.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD2227 5prime, mRNA sequence.	Drosophila melanogaster	39,855	25-Nov-98

**TABLE 4: ALIGNMENT RESULTS**

rx01989	630	GB_BA1:BSPGIA	1622	X16639	Bacillus stearothermophilus pgIA gene for phosphoglucoisomerase isoenzyme A (ECB <b>Bacillus stearothermophilus</b> 5.3.1.9).	66,292	20-Apr-95
		GB_BA1:BSUB0017	217420	299120	Bacillus subtilis complete genome (section 17 of 21): from 3197001 to 3414420.	37,255	26-Nov-97
		GB_BA2:AF132127	8452	AF132127	Streptococcus mutans sorbitol phosphoenolpyruvate:sugar phosphotransferase operon, complete sequence and unknown gene.	63,607	28-Sep-99
rx02026	720	GB_BA1:SXSCRBA	3161	X67744	S. <i>Xyleus</i> <i>scrB</i> and <i>scrR</i> genes.	67,778	28-Nov-96
		GB_BA1:BSUB0020	212150	299123	Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.	35,574	26-Nov-97
		GB_BA1:BSGENR	97015	X73124	B. <i>subtilis</i> genomic region (325 to 333).	51,826	2-Nov-93
rx02028	526	GB_BA1:MTC1237	27030	Z94752	Mycobacterium tuberculosis H37Rv complete genome; segment 46/162.	54,476	17-Jun-98
		GB_PL2:SC9537	66030	U87778	Saccharomyces cerevisiae chromosome V cosmid 9537, 9381, 9495, 9867, and lambda clone 5898.	36,190	1-Aug-97
		GB_GSS13:AO501177	767	AQ501177	V26G9 mTn-3xHA/lacZ Insertion Library Saccharomyces cerevisiae genomic 5' genomic survey sequence.	32,039	29-Apr-99
rx02054	1140	GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	61,896	27-Aug-99
		GB_BA1:MTY13E12	43401	Z95390	Mycobacterium tuberculosis H37Rv complete genome; segment 147/162.	59,984	17-Jun-98
		GB_BA1:MTU43540	3453	U43540	Mycobacterium tuberculosis rbaA, rhamnose biosynthesis protein (rba), and rmlC genes, complete cds.	59,629	14-Aug-97
rx02056	2891	GB_PAT:EI4601	4394	E14601	Brevibacterium lactofermentum gene for alpha-ketoglutaric acid dehydrogenase.	Corynebacterium glutamicum	98,928
		GB_BA1:D84102	4394	D84102	Corynebacterium glutamicum DNA for 2-oxoglutarate dehydrogenase, complete cds.	Corynebacterium glutamicum	98,928
		GB_BA1:MTV006	24440	AL021006	Mycobacterium tuberculosis H37Rv complete genome; segment 54/162.	Mycobacterium tuberculosis	39,265
		GB_HTG7:AC0055883	211682	AC0055833	Homo sapiens chromosome 17 clone RP-1-95E11 map 17, *** SEQUENCING IN Homo sapiens	37,453	08-DEC-1999
		GB_PL2:ATAC003033	84254	AC003033	PROGRESS *** 2 ordered pieces.		
		GB_PL2:ATAC002334	75050	AC002334	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711
		GB_EST38:AW028530	444	AW028530	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711
rx02061	1617	GB_BA1:HTG7:AC0055883	211682	AC0055833	Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711
		GB_PL2:ATAC003033	84254	AC003033	Arabidopsis thaliana chromosome II BAC F25I18 genomic sequence, complete sequence.	Arabidopsis thaliana	37,711
		GB_BA1:SCGLGC	1518	X89733	S.coelicolor DNA for glgc gene.	Streptomyces coelicolor	56,972
		GB_GSS4:AO687350	786	AQ687350	nbxb0074H11_CUGI Rice BAC Library Oryza sativa genomic clone nbxb0074H11r, Oryza sativa genomic survey sequence.	Oryza sativa	40,696
		GB_EST38:AW028530	444	AW028530	nbxb0074H11_NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2530795 3' similarHomo sapiens to WP:T03G11.6 CE04874_ mRNA sequence.	Homo sapiens	36,795
		GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	Mycobacterium tuberculosis	40,156
		GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	Mycobacterium tuberculosis	55,218
		GB_BA1:SCC0001205	9389	AJ001205	Streptomyces coelicolor A3(2) glycogen metabolism cluster!.	Streptomyces coelicolor	38,475
		GB_BA1:D90858	13548	D90858	E.coli genomic DNA, Kohara clone #401(51.3-51.6 min.).	Escherichia coli	38,586
		GB_EST37:AI948595	469	AI948595	wq0712.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2470583 3' mRNA sequence.	Homo sapiens	37,239
		GB_HTG3:AC010387	220665	AC010387	Homo sapiens chromosome 5 clone C1TB-H1_2074D8, *** SEQUENCING IN PROGRESS *** 77 unordered pieces.	Homo sapiens	38,868
		GB_BA1:MSGB1551CS	36548	L78813	Mycobacterium leprae cDNA sequence.	Mycobacterium leprae	51,399
		GB_BA1:MSGB1554CS	35548	L78814	Mycobacterium leprae cDNA sequence.	Mycobacterium leprae	51,399
		GB_ROAOF093099	2482	AF093099	Mus musculus transcription factor TBLYM (Tblym) mRNA, complete cds.	Mus musculus	36,683
rx02122	822	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	57,292
		GB_BA1:SC6G10	35734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,058

**TABLE 4: ALIGNMENT RESULTS**

				Pseudomonas putida	
rx02143	1011	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.
		GB_BA1:MSGGB1551CS	365548	L78813	Mycobacterium leprae cosmid B1551 DNA sequence.
		GB_BA1:MSGGB1554CS	365548	L78814	Mycobacterium leprae cosmid B1554 DNA sequence.
rx02144	1347	GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.
		GB_HTG3:AC011500_0	3000851	AC011500	Homo sapiens chromosome 19 clone C1T978SKB_60E11, *** SEQUENCING IN PROGRESS ***. 246 unordered pieces.
		GB_HTG3:AC011500_0	3000851	AC011500	Homo sapiens chromosome 19 clone C1T978SKB_60E11, *** SEQUENCING IN PROGRESS ***. 246 unordered pieces.
rx02147	1140	GB_EST28:AI492095	485	AI492095	[g07ta01:x1 NC1_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2103040 3', mRNA sequence.
		GB_EST10:AA157467	376	AA157467	z050e01:r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.
		GB_EST10:AA157467	376	AA157467	z050e01:r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590328 5', mRNA sequence.
rx02149	1092	GB_PR3:H5BK277P6	61698	AL117347	Human DNA sequence from clone 277P6 on chromosome 1q25.3-31.2, complete sequence.
		GB_BA2:EMB065R075	360	AF116423	Rhizobium etli mutant MB045 RosR-transcriptionally regulated sequence.
		GB_EST34:AI789323	574	AI789323	uk63305.y1 Sugano mouse kidney mka Mus musculus cDNA clone IMAGE:1972760Mus musculus 5' similar to WP-K11H12.8 CE12160 ; mRNA sequence.
rx02175	1416	GB_BA1:CGGLTG	3013	X66112	C. glutamicum glt gene for citrate synthase and ORF.
		GB_BA1:MTCY31	37630	Z73101	Mycobacterium tuberculosis H37Rv complete genome; segment 41/162.
		GB_BA1:MLCB57	38029	Z99494	Mycobacterium leprae cosmid E57.
rx02196	816	GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete Rattus norvegicus cds.
		GB_GSS8:AO012162	763	AQ012162	127FB037070-197 Cosmid library of chromosome II Rhodobacter sphaeroides genomic clone 127FB037070197, genomic survey sequence.
		GB_RO:RATDAPRP	2819	M76426	Rattus norvegicus dipeptidyl aminopeptidase-related protein (dpp6) mRNA, complete Rattus norvegicus cds.
rx02209	1694	GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.
		GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GII/10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (mavR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.
		GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.
		GB_BA1:AB025424	2995	AB025424	Corynebacterium glutamicum gene for aconitase, partial cds.
		GB_BA1:MTV007	32806	AL021184	Mycobacterium tuberculosis H37Rv complete genome; segment 64/162.
		GB_BA2:AF002133	15437	AF002133	Mycobacterium avium strain GII/10 transcriptional regulator (mav81) gene, partial cds, aconitase (acn), invasin 1 (inv1), invasin 2 (inv2), transcriptional regulator (mavR), ketoacyl-reductase (fabG), enoyl-reductase (inhA) and ferrochelatase (mav272) genes, complete cds.

**TABLE 4: ALIGNMENT RESULTS**

rxa02245	780	GB_BA2:RCU23145	5960	U23145	Rhodobacter capsulatus Calvin cycle carbon dioxide fixation operon: fructose-1,6-/sedoheptulose-1,7-bisphosphate aldolase (cbbA) gene, partial cds. Form II ribulose-1,5-bisphosphate carboxylase/oxygenase (cbbM) gene, complete cds, and Calvin cycle operon; pentose-5-phosphate-3-epimerase (cbbE), phosphoglycolate phosphatase (cbbZ), and cbbY genes, complete cds.	Escherichia coli	48,701	28-OCT-1997
		GB_BA1:ECU82664	139818	U82664	Escherichia coli minutes 9 to 11 genomic sequence.	Escherichia coli	39,119	11-Jan-97
		GB_HTG2:AC007922	158858	AC007922	Homo sapiens chromosome 18 clone hRPK.178_F_10 map 18, *** SEQUENCING IN PROGRESS ***; 11 unordered pieces.	Homo sapiens	33,118	26-Jun-99
rxa02256	1125	GB_BA1:CGGAPPKGK	3804	X59403	C:glutamic acid, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,289	05-OCT-1992
		GB_BA1:SCC54	30753	AL035591	Streptomyces coelicolor cosmid C54.	Streptomyces coelicolor	36,951	11-Jun-99
		GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	64,196	19-Jun-98
		GB_BA1:CGGAPPKGK	3804	X59403	C:glutamic acid, gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	98,873	05-OCT-1992
		GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	61,273	19-Jun-98
rxa02257	1338	GB_BA2:MAU82749	2530	U82749	Mycobacterium avium glyceraldehyde-3-phosphate dehydrogenase homolog (gapdh) gene, complete cds; and phosphoglycerate kinase gene, partial cds.	Mycobacterium avium	61,772	6-Jan-98
		GB_BA1:CGGAPPKGK	3804	X59403	C:glutamic acid, gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase.	Corynebacterium glutamicum	99,667	05-OCT-1992
		GB_BA1:CORPEPC	4885	M25819	C:glutamic acid, phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
		GB_PATA09073	4885	A09073	C:glutamic acid, ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
rxa02259	2895	GB_BA1:CORPEPC	4885	M25819	C:glutamic acid, phosphoenolpyruvate carboxylase gene, complete cds.	Corynebacterium glutamicum	100,000	15-DEC-1995
		GB_PATA09073	4885	A09073	C:glutamic acid, ppg gene for phosphoenol pyruvate carboxylase.	Corynebacterium glutamicum	100,000	25-Aug-93
		GB_BA1:CGPPC	3292	X14234	Corynebacterium glutamicum phosphoenolpyruvate carboxylase gene (EC 4.1.1.31), Corynebacterium glutamicum	Corynebacterium glutamicum	99,827	12-Sep-93
rxa02288	969	GB_PR3:HSDJ94E24	243145	AL050317	Human DNA sequence from clone RP1-94E24 on chromosome 20q12, complete sequence.	Homo sapiens	36,039	03-DEC-1999
		GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99
		GB_HTG3:AC010091	159526	AC010091	Homo sapiens clone NH0295A01, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Homo sapiens	35,331	11-Sep-99
rxa02292	798	GB_BA2:AF125164	26443	AF125164	Bacteroides fragilis 638R polysaccharide B (PS B2) biosynthesis locus, complete sequence; and unknown genes.	Bacteroides fragilis	39,747	01-DEC-1999
		GB_GSS5:AQ744695	827	AQ744695	HS_5505_A2_C06_SP6 RPC1-11 Human Male BAC Library clone Plate=1081 Col=12 Row=E, genomic survey sequence.	Homo sapiens	39,185	16-Jul-99
		GB_EST14:AA381925	309	AA381925	EST95058 Activated T-cells I Homo sapiens cDNA 5' end, mRNA sequence.	Homo sapiens	35,922	21-Apr-97
		GB_BA1:MTCY2268	22550	Z95858	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	57,677	17-Jun-98
		GB_BA1:MTCY2268	22550	Z95858	Mycobacterium tuberculosis H37Rv complete genome; segment 49/162.	Mycobacterium tuberculosis	37,143	17-Jun-98
rxa02326	939	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998
		GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997
		GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis	37,363	17-Jun-98	
rxa02327	1083	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	99,259	08-MAY-1998
		GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	99,259	24-DEC-1997
		GB_BA1:MTCY349	43523	Z83018	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162.	Mycobacterium tuberculosis	41,317	17-Jun-98

**TABLE 4: ALIGNMENT RESULTS**

rxa02328	1719	GB_BA1:CGPYC	3728	Y09548	Corynebacterium glutamicum pyc gene.	Corynebacterium glutamicum	100,000	08-MAY-1998
		GB_BA2:AF038548	3637	AF038548	Corynebacterium glutamicum pyruvate carboxylase (pyc) gene, complete cds.	Corynebacterium glutamicum	100,000	24-DEC-1997
		GB_PL2:AF097728	3916	AF097728	Aspergillus terreus pyruvate carboxylase (Pyc) mRNA, complete cds.	Aspergillus terreus	52,248	29-OCT-1998
		GB_BA1:MSGLTA	1776	X60513	M.smegeatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,460	20-Sep-91
		GB_BA2:ABU85944	1334	U85944	Antarctic bacterium DS2-3R citrate synthase (cisy) gene, complete cds.	Antarctic bacterium DS2-3R	57,154	23-Sep-97
		GB_BA2:AE000175	15067	AE000175	Escherichia coli K-12 MG1655 section 65 of 400 of the complete genome.	Escherichia coli	38,164	12-Nov-98
		GB_BA1:MSGLTA	1776	X60513	M.smegeatis gltA gene for citrate synthase.	Mycobacterium smegmatis	58,929	20-Sep-91
		GB_PR4:HJAC002299	171681	AC002299	Homo sapiens Chromosome 16 BAC clone C1T987-SKA-113A6 ~complete genomic Homo sapiens sequence, complete sequence.	Homo sapiens	33,070	23-Nov-98
		GB_HTG2:AC007889	127840	AC007889	Drosophila melanogaster chromosome 3 clone BACR48E12 (D695) RPCI-98 48.E.12 map 87A-87B strain y; cn bw sp; *** SEQUENCING IN PROGRESS***,	Drosophila melanogaster	34,897	2-Aug-99
					48.E.12 map 87A-87B strain y; cn bw sp; *** SEQUENCING IN PROGRESS***,			
rxa02399	1467	GB_BA1:CCACEA	2427	X75504	C. glutamicum aceA gene and thiX genes (partial).	Corynebacterium glutamicum	100,000	9-Sep-94
		GB_BA1:CORACEA	1905	L28760	Corynebacterium glutamicum isocitrate lyase (aceA) gene.	Corynebacterium glutamicum	100,000	10-Feb-95
		GB_PAT:1M3693	2135	I13693	Sequence 3 from patent US 5439822.	Unknown.	99,795	26-Sep-95
		GB_BA1:CCACEB	3024	X78491	C. glutamicum (ATCC 13032) aceB gene.	Corynebacterium glutamicum	99,914	13-Jan-95
		GB_BA1:CORACEB	2725	L27123	Corynebacterium glutamicum malate synthase (aceB) gene, complete cds.	Corynebacterium glutamicum	99,786	8-Jun-95
		GB_BA1:PFFC2	5588	Y11998	P.fluorescens FC2.1, FC2.2, FC2.3C, FC2.4 and FC2.5c open reading frames.	Pseudomonas fluorescens	63,539	11-Jul-97
		GB_PR4:AC007102	176258	AC007102	Homo sapiens chromosome 4 clone C0162P16 map 4p16, complete sequence.	Homo sapiens	35,069	2-Jun-99
		GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
		GB_HTG3:AC011214	183414	AC011214	Homo sapiens clone 5_C_3, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	36,885	03-OCT-1999
		GB_BA2:AF101055	7457	AF101055	Clostridium acetobutylicum atp operon, complete sequence.	Clostridium acetobutylicum	39,605	03-MAR-1999
		GB_OM:RABPKA	4441	J03247	Rabbit phosphorylase kinase (alpha subunit) mRNA, complete cds.	Oryctolagus cuniculus	36,061	27-Apr-93
		GB_OM:RABPLASM	4458	M64656	Oryctolagus cuniculus phosphotyrosine kinase alpha subunit mRNA, complete cds.	Oryctolagus cuniculus	36,000	22-Jun-98
rxa02440	963	GB_EST14:AA417723	374	AA417723	IMAGE:746207 3' similar Homo sapiens to contains Alu repetitive element; contains element L1 repetitive element; mRNA sequence.	Homo sapiens	38,770	16-OCT-1997
		GB_EST11:AA215428	303	AA215428	zr95a07_s1 NCL_OGAP_GCB1 Homo sapiens cDNA clone IMAGE:683412 3' similar Homo sapiens to contains Alu repetitive element; mRNA sequence.	Homo sapiens	39,934	13-Aug-97
		GB_BA1:MTCY77	22255	Z95389	Mycobacterium tuberculosis H37Rv complete genome; segment 146/162.	Mycobacterium tuberculosis	38,889	18-Jun-98
		GB_EST14:AA426336	375	AA426336	zv53g02_s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:7.57394 3', mRNA sequence.	Homo sapiens	38,043	16-OCT-1997
		GB_BA1:STMACC8	1353	M55426	S.fradiae aminoglycoside acetyltransferase (aacC8) gene, complete cds.	Streptomyces fradiae	37,097	05-MAY-1993
		GB_PR3:AC004500	77538	AC004500	Homo sapiens chromosome 5, P1 clone 1076B9 (LBNL H14), complete sequence.	Homo sapiens	33,256	30-MAR-1998
rxa02453	876	GB_BA1:AB009078	2686	AB009078	Brevibacterium saccharolyticum gene for L-2,3-butenediol dehydrogenase, complete Brevibacterium saccharolyticum cds.	Brevibacterium saccharolyticum	95,990	13-Feb-99
		GB_OM:BTU1200	877	U71200	Bos taurus acetoin reductase mRNA, complete cds.	Bos taurus	51,659	8-Oct-97
		GB_EST2:F12685	287	F12685	HSC3DA031 normalized infant brain cDNA Homo sapiens cDNA clone c-3da03, mRNA sequence	Homo sapiens	41,509	14-Mar-95
rxa02480	1779	GB_BA1:MTV012	70287	AL021287	Mycobacterium tuberculosis H37Rv complete genome; segment 132/162.	Mycobacterium tuberculosis	36,737	23-Jun-99
		GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	35,511	24-MAR-1999
		GB_BA1:AP000060	347800	AP000060	Aeropyrum pernix genomic DNA, section 3/7.	Aeropyrum pernix	48,014	22-Jun-99
rxa02485								

TABLE 4: ALIGNMENT RESULTS

rx02492	840	GB_BA1:STMPGM	921	M83661	Streptomyces coelicolor phosphoglycerate mutase (PGM) gene, complete cds.	65,672	26-Apr-93
		GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium leprae cosmid B2168.	61,436	17-Jun-98
		GB_BA1:U00018	42991	U00018	Mycobacterium leprae	37,893	01-MAR-1994
rx02528	1098	GB_PR2:HS161N10	56075	AL008707	Human DNA sequence from PAC 161N10 on chromosome X:25. Contains EST.	37,051	23-Nov-99
		GB_HTG2:AC008235	136017	AC008235	15.B.19 map 94F-95A strain 'y' cn bw sp. *** SEQUENCING IN PROGRESS *** , 125 unorderd pieces.	36,822	2-Aug-99
		GB_HTG2:AC008235	136017	AC008235	Drosophila melanogaster chromosome 3 clone BACR15B19 (D995) RPCI-98 unorderd pieces.	36,822	2-Aug-99
rx02539	1641	GB_BA2:RSU17129	17425	U17129	15.B.19 map 94F-95A strain 'y' cn bw sp. *** SEQUENCING IN PROGRESS*** , 125 unorderd pieces.	66,117	16-Jul-99
		GB_BA1:MTV038	16094	AL021933	Rhodococcus erythropolis ThcA (thcA) gene, complete cds; and unknown genes.	65,174	17-Jun-98
		GB_BA2:AF068264	3152	AF068264	Mycobacterium tuberculosis H37Rv complete genome; segment 24/162. Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA)gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinoline quinone synthesis A (pqqA) genes, complete cds; and pyrroloquinoline quinone synthesis B (pqqB) gene, partial cds.	65,448	18-MAR-1999
rx02551	483	GB_BA1:BACHUTWAPA28954	17057	D29985	Bacillus subtilis wpaA and orf genes for wall-associated protein and hypothetical proteins.	53,602	7-Feb-99
		GB_BA1:BSGBGLUC	4290	Z34526	Bacillus subtilis (Marburg 168) genes for beta-glucoside permease and beta-glucosidase.	53,602	7-Feb-99
rx02556	1281	GB_HTG3:AC008128	335761	AC008128	Homo sapiens, *** SEQUENCING IN PROGRESS *** , 106 unorderd pieces.	34,022	22-Aug-99
		GB_HTG3:AC008128	335761	AC008128	Homo sapiens, *** SEQUENCING IN PROGRESS *** , 106 unorderd pieces.	34,022	22-Aug-99
		GB_PI2:AC005292	90053	AC005292	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence.	33,858	16-Apr-99
rx02560	990	GB_IN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	36,420	2-Sep-99
		GB_EST32:AT731605	566	A1731605	BNI:GHI0201 Six-day Cotton fiber Grossypium hirsutum cDNA 5' similar to (AC04684) hypothetical protein [Arabidopsis thaliana], mRNA sequence.	38,095	11-Jun-99
		GB_IN1:CEF07A11	35692	Z66511	Caenorhabditis elegans cosmid F07A11, complete sequence.	33,707	2-Sep-99
rx02572	668	GB_BA1:MTCY63	38900	Z96600	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	61,677	17-Jun-98
		GB_BA1:MTCY63	38900	Z96600	Mycobacterium tuberculosis H37Rv complete genome; segment 16/162.	37,170	17-Jun-98
		GB_HTG1:HS24H01	46989	AL121632	Homo sapiens chromosome 21 clone LNLC11H0124 map 21q21, *** SEQUENCING IN PROGRESS *** , in unorderd pieces.	19,820	29-Sep-98
rx02596	1326	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	36,957	24-Jun-99
		GB_BA2:AF026540	1778	AF026540	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	67,627	30-OCT-1998
		GB_BA2:MTU96128	1200	U96128	Mycobacterium tuberculosis UDP-galactopyranose mutase (glf) gene, complete cds.	70,417	25-MAR-1998
rx02611	1775	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	38,532	17-Jun-98
		GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	60,575	10-DEC-1996
		GB_BA1:U00014	36470	U00014	Mycobacterium leprae cosmid B1349.	57,486	29-Sep-94
rx02612	2316	GB_BA1:MTCY130	32514	Z73902	Mycobacterium tuberculosis H37Rv complete genome; segment 59/162.	38,018	17-Jun-98
		GB_BA1:MSGY151	37036	AD000018	Mycobacterium tuberculosis sequence from clone y151.	58,510	10-DEC-1996

**TABLE 4: ALIGNMENT RESULTS**

GB_BA1:STM/GIGEN	2557	L11647	Streptomyces aureofaciens glycogen branching enzyme (gjb) gene, complete cds.	<i>Streptomyces aureofaciens</i>	57,193	25-MAY-1995
GB_BA1:CGL133719	1839	AJ133719	Corynebacterium glutamicum ycc gene, amrR gene and citE gene, partial.	<i>Corynebacterium glutamicum</i>	36,858	12-Aug-99
GB_IN1:CEM106	398973	246935	Caenorhabditis elegans cosmid M106, complete sequence.	<i>Caenorhabditis elegans</i>	37,608	2-Sep-99
GB_EST29:AI547662	377	AI547662	UI-R-C3-sz-h-03-0-U1.s1 UI-R-C3 Rattus norvegicus cDNA clone UI-R-C3-sz-h-03-0-Rattus norvegicus UI 3', mRNA sequence.	<i>Rattus norvegicus</i>	50,667	3-Jul-99
GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	<i>Mycobacterium tuberculosis</i>	39,187	24-Jun-99
GB_BA1:PAU496666	4495	U496666	Pseudomonas aeruginosa (orfX), glycerol diffusion facilitator (gpf), glycerol kinase (gpk), and Gip repressor (gpr) genes, complete cds, and (orfX) gene, partial cds.	<i>Pseudomonas aeruginosa</i>	59,273	18-MAY-1997
GB_BA1:AB015974	1641	AB015974	Pseudomonas tolasaki gfpK gene for glycerol kinase, complete cds.	<i>Pseudomonas tolasaki</i>	58,339	28-Aug-99
GB_EST6:N657877	512	NG67877	20827 Lambda-PR1.2 Arabidopsis italiana cDNA clone 232BTT7, mRNA sequence.	<i>Arabidopsis italiana</i>	39,637	5-Jan-98
GB_PL2:T17H3	65839	AC005916	Arabidopsis italiana chromosome 1 BAC T17H3 sequence, complete sequence.	<i>Arabidopsis italiana</i>	33,735	5-Aug-99
GB_RO:MMU58105	88871	U55105	Mus musculus Btk locus, alpha-D-galactosidase A (Ags), ribosomal protein (L44L), and Bruton's tyrosine kinase (Btk) genes, complete cds.	<i>Mus musculus</i>	35,431	13-Feb-97
GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	<i>Homo sapiens</i>	38,851	01-MAY-1998
GB_PR3:AC004643	43411	AC004643	Homo sapiens chromosome 16, cosmid clone 363E3 (LANL), complete sequence.	<i>Homo sapiens</i>	41,599	01-MAY-1998
GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutamylphosphate reductase (argC), ornithine/Corynebacterium glutamicum transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	<i>Corynebacterium glutamicum</i>	40,413	1-Jul-98
GB_BA1:PDENQOURF	10425	L02354	Paracoccus denitrificans NADH dehydrogenase (UFR4), (NQO9), (NQO5), (UFR5), (NQO6), (NQO10), (NQO11), (NQO12), (NQO13), and (NQO14) genes, complete cds's; biotin [acetyl-CoA carboxyl] ligase (blrA) gene, complete cds.	<i>Paracoccus denitrificans</i>	40,735	20-MAY-1993
GB_BA1:MTCY339	42861	Z77163	Mycobacterium tuberculosis H37Rv complete genome; segment 101/162.	<i>Mycobacterium tuberculosis</i>	36,471	17-Jun-98
GB_BA1:MXQDEVRS	2452	L19029	Myxococcus xanthus devR and devS genes, complete cds's.	<i>Myxococcus xanthus</i>	38,477	27-Jan-94
GB_BA1:BACLDH	1147	M13394	B.caedoliticus lactate dehydrogenase (LDH) gene, complete cds.	<i>Bacillus caedoliticus</i>	57,371	26-Apr-93
GB_BA1:BACLDHL	1361	M14788	B.stearothermophilus lct gene encoding L-lactate dehydrogenase, complete cds.	<i>Bacillus stearothermophilus</i>	57,277	26-Apr-93
GB_PAT:AE6664	1350	A06664	B.stearothermophilus lct gene.	<i>Bacillus stearothermophilus</i>	57,277	29-Jul-93
GB_EST15:AA494626	121	AA494626	f09d04_r1 Zebrafish ICRFzfis Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 GTT-MISMATCH BINDING PROTEIN .; mRNA sequence.	<i>Danio rerio</i>	50,746	27-Jun-97
GB_EST15:AA494626	121	AA494626	f09d04_r1 Zebrafish ICRFzfis Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 GTT-MISMATCH BINDING PROTEIN .; mRNA sequence.	<i>Danio rerio</i>	36,364	27-Jun-97
GB_EST19:AA758660	233	AA758660	ah67d06_s1 Soares testis_NHT Homo sapiens cDNA clone 1320683 3', mRNA sequence.	<i>Homo sapiens</i>	37,059	29-DEC-1998
GB_EST15:AA494626	121	AA494626	fa09d04_r1 Zebrafish ICRFzfis Danio rerio cDNA clone 11A22 5' similar to TR:G1171163 G1171163 GTT-MISMATCH BINDING PROTEIN .; mRNA sequence.	<i>Danio rerio</i>	42,149	27-Jun-97

**TABLE 4: ALIGNMENT RESULTS**

rx02737	1685	GB_PR4:AC006285	150172	AC006285	Homo sapiens, complete sequence.	Homo sapiens	37,655		
		GB_PAT:E13665	2260	E13655	9 DNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	99,580		
		GB_BA1:MTCY493	40790	Z95844	Mycobacterium tuberculosis H37Rv complete genome; segment 63/162.	Mycobacterium tuberculosis	38,363		
		GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	39,444		
		GB_PAT:E13655	2260	E13655	9 DNA encoding glucose-6-phosphate dehydrogenase.	Corynebacterium glutamicum	98,226		
		GB_BA1:SCC22	22115	AL096839	Streptomyces coelicolor cosmid C22.	Streptomyces coelicolor	60,399		
		GB_BA1:SC5A7	40337	AL031107	Streptomyces coelicolor cosmid 5A7.	Streptomyces coelicolor	12,399		
		GB_BA1:AB023377	2572	AB023377	Corynebacterium glutamicum tkt gene for transketolase, complete cds.	Corynebacterium glutamicum	27,398		
		GB_BA1:MLCL536	36224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	99,640		
		GB_BA1:J00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	61,573		
		GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48I10 (D505) RPCI-98 48.I.10 Drosophila melanogaster map 49E6-49F8 strain y, cn bw sp. *** SEQUENCING IN PROGRESS *** , 17 unordered pieces.	Drosophila melanogaster	37,105		
		GB_HTG2:AC006247	174368	AC006247	Drosophila melanogaster chromosome 2 clone BACR48I10 (D505) RPCI-98 48.I.10 Drosophila melanogaster map 49E6-49F8 strain y, cn bw sp. *** SEQUENCING IN PROGRESS *** , 17 unordered pieces.	Drosophila melanogaster	37,105		
		GB_HTG3:AC007150	121474	AC007150	Drosophila melanogaster chromosome 2 clone BACR16P13 (D597) RPCI-98 16.P.13 map 49E-49F strain y, cn bw sp. *** SEQUENCING IN PROGRESS *** , 87 unordered pieces.	Drosophila melanogaster	2-Aug-99		
		rx02741	1089	GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022 14, *** SEQUENCING IN PROGRESS *** , 14	Homo sapiens	33,116
		GB_HTG2:AC004951	129429	AC004951	Homo sapiens clone DJ1022 14, *** SEQUENCING IN PROGRESS *** , 14	Homo sapiens	33,116		
		GB_INI:AB006546	931	AB006546	Ephydalia fluviatilis mRNA for G protein a subunit 4, partial cds.	Ephydalia fluviatilis	36,379		
		GB_BA1:MLCL536	35224	Z99125	Mycobacterium leprae cosmid L536.	Mycobacterium leprae	48,401		
		GB_BA1:J00013	35881	U00013	Mycobacterium leprae cosmid B1496.	Mycobacterium leprae	48,401		
		GB_HTG2:AC007401	83657	AC007401	Homo sapiens clone NH0501007, *** SEQUENCING IN PROGRESS *** , 3	Homo sapiens	37,128		
		rx02797	1026	GB_BA1:CGBBETPGEN	2339	X93514	C(glutamicum betP gene.	Corynebacterium glutamicum	38,889
		GB_GSS9:Q148714	405	AQ148714	HS_3136_A1_A03 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=5 Row=A, genomic survey sequence.	Homo sapiens	34,321		
		GB_BA1:BFU64514	3837	U64514	Bacillus firmus dppABC operon, dipeptide transporter protein dppA gene, partial cds, and dipeptide transporter proteins dppB and dppC genes, complete cds.	Bacillus firmus	8-Sep-97		
		GB_BA1:J00020	36947	U00020	Mycobacterium leprae cosmid B229.	Mycobacterium leprae	38,072		
		GB_BA2:PSU85643	4032	U85643	Pseudomonas syringae pv. syringae putative dihydroterotate synthase gene, partial Pseudomonas syringae pvi.	Pseudomonas syringae	1-Feb-97		
					protein SecG (secG), tRNA-Leu, tRNA-Met, and 15 kDa protein genes, complete cds.	tRNA-Met, and 15 kDa protein genes,	34,462		
		GB_BA1:SC6G4	41055	AL031317	Streptomyces coelicolor cosmid 6G4.	Streptomyces coelicolor	59,314		
		GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS *** , 12 unordered pieces.	Homo sapiens	20-Aug-98		
		GB_HTG2:AC008105	91421	AC008105	Homo sapiens chromosome 17 clone 2020_K_17 map 17, *** SEQUENCING IN PROGRESS *** , 12 unordered pieces.	Homo sapiens	22-Jul-99		
		GB_EST33:AV117143	222	AV117143	AV117143 Mus musculus C57BL/6J 10-day embryo Mus musculus cDNA clone 261020017, mRNA sequence.	Mus musculus	37,607		
							30-Jun-99		

**TABLE 4: ALIGNMENT RESULTS**

rx02829	373	GB-HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LLOXNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
		GB-HTG1:HSU9G8	48735	AL008714	Homo sapiens chromosome X clone LLOXNC01-9G8, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	41,595	23-Nov-99
		GB_PR3:HSU85B5	39550	Z69724	Human DNA sequence from cosmid U85B5, between markers DXS368 and DXS87 on chromosome X.	Homo sapiens	41,595	23-Nov-99
rx03216	1141	GB-HTG3:AC008184	151720	AC008184	Drosophila melanogaster chromosome 2 clone BACR04D05 (D540) RPCI-98 04.D.5 Drosophila melanogaster map 36E5-36F2 strain Y, cn bw sp, *** SEQUENCING IN PROGRESS **, 27 unordered pieces.	Drosophila melanogaster	39,600	2-Aug-99
		GB_EST15:AA477537	411	AA477537	ZU06g12.r1 Soates ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740134 Homo sapiens 5' similar to contains Alu repetitive element;contains element HGR repetitive element , mRNA sequence.	Homo sapiens	37,260	9-Nov-97
		GB_EST26:AI330662	412	AI330662	fa91d08.y1 zebrafish fin day1 regeneration Danio rerio cDNA 5', mRNA sequence.	Danio rerio	37,805	28-DEC-1998
rx03215	1038	GB_BA1:SC3F9	19830	AL023862	Streptomyces coelicolor cosmid 3F9.	Streptomyces coelicolor A3(2)	48,657	10-Feb-99
		GB_BA1:SLLINC	36270	X79146	S.lincolnensis (78-11) Lincomycin production genes.	Streptomyces lincolnensis	39,430	15-MAY-1996
		GB-HTG5:AC009660	204320	AC009660	Homo sapiens chromosome 15 clone RP11-424J10 map 15, *** SEQUENCING IN PROGRESS **, 41 unordered pieces.	Homo sapiens	35,151	04-DEC-1999
rx03224	1288	GB_PR3:AC004076	41322	AC004076	Homo sapiens chromosome 19, cosmid R30217, complete sequence.	Homo sapiens	37,788	29-Jan-98
		GB_PL2:SPAC926	23193	AL110469	S.pombe chromosome 1 cosmid c926.	Schizosaccharomyces pombe	38,474	2-Sep-99
		GB_BA2:AE001081	11473	AE001081	Archaeoglobus fulgidus section 26 of 172 of the complete genome.	Archaeoglobus fulgidus	35,871	15-DEC-1997